

Sequence Listing

- <110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> P2830P1C52
- <150> 09/946374
<151> 2001-09-04
- <150> 60/098716
<151> 1998-09-01
- <150> 60/098723
<151> 1998-09-01
- <150> 60/098749
<151> 1998-09-01
- <150> 60/098750
<151> 1998-09-01
- <150> 60/098803
<151> 1998-09-02
- <150> 60/098821
<151> 1998-09-02
- <150> 60/098843
<151> 1998-09-02
- <150> 60/099536
<151> 1998-09-09
- <150> 60/099596
<151> 1998-09-09

<151> 1998-09-17
 <150> 60/100684
 <151> 1998-09-17
 <150> 60/100710
 <151> 1998-09-17
 <150> 60/100711
 <151> 1998-09-17
 <150> 60/100848
 <151> 1998-09-18
 <150> 60/100849
 <151> 1998-09-18
 <150> 60/100919
 <151> 1998-09-17
 <150> 60/100930
 <151> 1998-09-17
 <150> 60/101014
 <151> 1998-09-18
 <150> 60/101068
 <151> 1998-09-18
 <150> 60/101071
 <151> 1998-09-18
 <150> 60/101279
 <151> 1998-09-22
 <150> 60/101471
 <151> 1998-09-23
 <150> 60/101472
 <151> 1998-09-23
 <150> 60/101474
 <151> 1998-09-23
 <150> 60/101475
 <151> 1998-09-23
 <150> 60/101476
 <151> 1998-09-23
 <150> 60/101477
 <151> 1998-09-23
 <150> 60/101479
 <151> 1998-09-23
 <150> 60/101738
 <151> 1998-09-24

<150> 60/105882
<151> 1998-10-27

<150> 60/106023
<151> 1998-10-28

<150> 60/106029
<151> 1998-10-28

<150> 60/106030
<151> 1998-10-28

<150> 60/106032
<151> 1998-10-28

<150> 60/106033
<151> 1998-10-28

<150> 60/106062
<151> 1998-10-27

<150> 60/106178
<151> 1998-10-28

<150> 60/106248
<151> 1998-10-29

<150> 60/106384
<151> 1998-10-29

<150> 60/108500
<151> 1998-10-29

<150> 60/106464
<151> 1998-10-30

<150> 60/106856
<151> 1998-11-03

<150> 60/106902
<151> 1998-11-03

<150> 60/106905
<151> 1998-11-03

<150> 60/106919
<151> 1998-11-03

<150> 60/106932
<151> 1998-11-03

<150> 60/106934
<151> 1998-11-03

<150> 60/107783
<151> 1998-11-10

<150> 60/108775

<151> 1998-11-17
 <150> 60/108779
 <151> 1998-11-17
 <150> 60/108787
 <151> 1998-11-17
 <150> 60/108788
 <151> 1998-11-17
 <150> 60/108801
 <151> 1998-11-17
 <150> 60/108802
 <151> 1998-11-17
 <150> 60/108806
 <151> 1998-11-17
 <150> 60/108807
 <151> 1998-11-17
 <150> 60/108848
 <151> 1998-11-18
 <150> 60/108849
 <151> 1998-11-18
 <150> 60/108850
 <151> 1998-11-18
 <150> 60/108851
 <151> 1998-11-18
 <150> 60/108852
 <151> 1998-11-18
 <150> 60/108858
 <151> 1998-11-18
 <150> 60/108867
 <151> 1998-11-17
 <150> 60/108904
 <151> 1998-11-18
 <150> 60/108925
 <151> 1998-11-17
 <150> 60/113296
 <151> 1998-12-22
 <150> 60/114223
 <151> 1998-12-30
 <150> 60/129674
 <151> 1999-04-16

<150> 60/141037
<151> 1999-06-23

<150> 60/144758
<151> 1999-07-20

<150> 60/145698
<151> 1999-07-26

<150> 60/162506
<151> 1999-10-29

<150> 09/218517
<151> 1998-12-22

<150> 09/284291
<151> 1999-04-12

<150> 09/403297
<151> 1999-10-18

<150> 09/872035
<151> 2001-06-01

<150> 09/882636
<151> 2001-06-14

<150> PCT/US99/00106
<151> 1999-01-05

<150> PCT/US99/20111
<151> 1999-09-01

<150> PCT/US99/21194
<151> 1999-09-15

<150> PCT/US99/28313
<151> 1999-11-30

<150> PCT/US99/28551
<151> 1999-12-02

<150> PCT/US99/30095
<151> 1999-12-16

<150> PCT/US00/00219
<151> 2000-01-05

<150> PCT/US00/00376
<151> 2000-01-06

<150> PCT/US00/03565
<151> 2000-02-11

<150> PCT/US00/04342
<151> 2000-02-18

<150> PCT/US00/05004

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Sequence - Artificial

<400> 1

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-41

<223> Sequence - Artificial

<400> 2

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3

ccaatcgccc ggtgcggtgg tgcagggtct cgggctagtc atggcgctccc 50
 cgtctcggag actgcagact aaaccagtca ttacttgttt caagagcgtt 100
 ctgctaattct acacttttat tttctggatc actggcggtta tccttcttgc 150
 agttggcatt tggggcaagg tgagcctgga gaattacttt tctcttttaa 200
 atgagaaggc caccaatgtc cccttcgtgc tcattgctac tggtagcgtc 250
 attattcttt tgggcacctt tgggtgtttt gctacctgcc gagcttctgc 300
 atggatgcta aaactgtatg caatgtttct gactctcgtt tttttggctg 350
 aactggctgc tgccatcgta ggatttggtt tcagacatga gattaagaac 400
 agctttaaga ataattatga gaaggctttg aagcagtata actctacagg 450
 agattataga agccatgcag tagacaagat ccaaaatacg ttgcattggt 500
 gtggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550
 aaaggatttc ctaagagttg ctgtaaaactt gaagattgta ctccacagag 600
 agatgcagac aaagtaaaca atgaaggttg ttttataaag gtgatgacca 650
 ttatagagtc agaaatggga gtcgttcgag gaatttcctt tggagttgct 700
 tgcttccaac tgattggaat ctttctcgcc tactgccwct ctcgtgccat 750

aacaaataac cagtatgaga tagtgtaacc caatgtatct gtgggcctat 800
 tcctctctac ctttaaggac atttagggtc cccctgtga attagaaagt 850
 tgcttggctg gagaactgac aacactactt actgatagac caaaaaacta 900
 caccagtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950
 ataggctgat tcaatcaaga tccgtgctcg cagtgggctg attcaatcaa 1000
 gatgtatgtt tgctatgttc taagtccacc ttctatccca ttcatgttag 1050
 atcgttgaaa cctgtatcc ctctgaaaca ctggaagagc tagtaaattg 1100
 taaatgaagt 1110

<210> 4
 <211> 245
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal Peptide

<220>
 <221> TRANSMEM
 <222> 19-42, 61-83, 92-114, 209-230
 <223> Transmembrane Domains

<220>
 <221> misc_feature
 <222> 69-80, 211-222
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 75-81, 78-84, 210-216, 214-220, 226-232
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 134-138
 <223> N-Glycosylation Site.

<220>
 <221> misc_feature
 <222> 160-168, 160-169
 <223> Tyrosine Kinase Phosphorylation Site.

<220>
 <221> unsure
 <222> 233
 <223> unknown amino acid

<400> 4
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr

1	5	10	15
Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile	20	25	30
Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser	35	40	45
Leu Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val	50	55	60
Pro Phe Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly	65	70	75
Thr Phe Gly Cys Phe Ala Thr Cys Arg Ala Ser Ala Trp Met Leu	80	85	90
Lys Leu Tyr Ala Met Phe Leu Thr Leu Val Phe Leu Val Glu Leu	95	100	105
Val Ala Ala Ile Val Gly Phe Val Phe Arg His Glu Ile Lys Asn	110	115	120
Ser Phe Lys Asn Asn Tyr Glu Lys Ala Leu Lys Gln Tyr Asn Ser	125	130	135
Thr Gly Asp Tyr Arg Ser His Ala Val Asp Lys Ile Gln Asn Thr	140	145	150
Leu His Cys Cys Gly Val Thr Asp Tyr Arg Asp Trp Thr Asp Thr	155	160	165
Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser Cys Cys Lys Leu	170	175	180
Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val Asn Asn Glu	185	190	195
Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu Met Gly	200	205	210
Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu Ile	215	220	225
Gly Ile Phe Leu Ala Tyr Cys Xaa Ser Arg Ala Ile Thr Asn Asn	230	235	240
Gln Tyr Glu Ile Val	245		

<210> 5
 <211> 1218
 <212> DNA
 <213> Homo sapiens

<400> 5
 cccacgcgtc cggcgccgtg gcctcgcgtc catctttgcc gttctctcgg 50

acctgtcaca aaggagtcgc gccgccgccg ccgccccctc cctccggtgg 100
 gcccgggagg tagagaaagt cagtgccaca gcccgaccgc gctgctctga 150
 gccctgggca cgcggaacgg gagggagtct gagggttggg gacgtctgtg 200
 agggagggga acagccgctc gagcctgggg cgggcggacc ggactggggc 250
 cggggtaggc tctggaaagg gcccgggaga gaggtggcgt tggtcagaac 300
 ctgagaaaca gccgagaggt tttccaccga ggcccgcgct tgagggatct 350
 gaagagggtc ctagaagagg gtgttccctc tttcgggggt cctcaccaga 400
 agaggttctt gggggtcgcc ctcttgagga ggctgcggct aacagggccc 450
 agaactgcca ttggatgtcc agaatcccct gtagttgata atgttgggaa 500
 taagctctgc aactttcttt ggcattcagt tgttaaaaac aaataggatg 550
 caaatctctc aactccaggt tatgaaaaca gtacttgga aactgaaaac 600
 tacctaaatg atcgtctttg gttggggcgt gttcttagcg agcagaagcc 650
 ttggccaggg tctgttggtg actctcgaag agcacatagc ccacttccta 700
 gggactggag gtgccgctac taccatgggt aattcctgta tctgccgaga 750
 tgacagtgga acagatgaca gtgttgacac ccaacagcaa caggccgaga 800
 acagtgcagt acccactgct gacacaagga gcccaaccacg ggaccctgtt 850
 cggccaccaa ggagggggccg aggacctcat gagccaagga gaaagaaaca 900
 aaatgtggat gggctagtgt tggacacact ggcagtaata cggactcttg 950
 tagataagta agtatctgac tcacggtcac ctccagtgga atgaaaagtg 1000
 ttctgcccgg aaccatgact ttaggactcc ttcagttcct ttaggacata 1050
 ctcgccaagc cttgtgtca caggggcaaag gagaatattt taatgctccg 1100
 ctgatggcag agtaaagat aagatttgat gtttttgctt gctgtcatct 1150
 actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaag 1200
 ctatgatctt tattagag 1218

<210> 6
 <211> 117
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-16
 <223> Signal Peptide

<220>
 <221> misc_feature
 <222> 18-24, 32-38, 34-40, 35-41, 51-57
 <223> N-Myristoylation Site.

 <220>
 <221> misc_feature
 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

<400> 6
 Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu
 1 5 10 15

 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe
 20 25 30

 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile
 35 40 45

 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60

 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75

 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
 80 85 90

 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu
 95 100 105

 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys
 110 115

<210> 7
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 7
 ggcacgaggc gctgtccacc cgggggcggt ggagtgaggt accagattca 50
 gcccatattg ccccgacgcc tctgttctcg gaatccgggt gctgcggatt 100
 gaggtcccgg ttcctaacgg actgcaagat ggaggaaggc gggaacctag 150
 gaggcctgat taagatggtc catctactgg tcttgtcagg tgccctggggc 200
 atgcaaagt gggtgacctt cgtctcaggc ttctgtcttt tccgaagcct 250
 tccccgacat accttcggac tagtgcagag caaactcttc cccttctact 300
 tccacatctc catgggctgt gccttcatca acctctgcat cttggcttca 350
 cagcatgctt gggctcagct cacattctgg gaggccagcc agctttacct 400
 gctgttctct agccttacgc tggccactgt caacgcccgc tggctggaac 450

cccgaccac agctgccatg tgggccctgc aaaccgtgga gaaggagcga 500
 ggctgggtg gggaggtacc aggcagccac cagggtcccg atccctaccg 550
 ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600
 tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650
 aatgggctct gtctcgctgg ccttgccctg gaaataagga gcctctagca 700
 tgggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750
 aaaaaa 756

<210> 8
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-24
 <223> Signal Peptide

<220>
 <221> misc_feature
 <222> 4-10, 5-11, 47-53, 170-176, 176-182
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 44-85
 <223> G-protein Coupled Receptors Proteins.

<220>
 <221> misc_feature
 <222> 54-65
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 82-86
 <223> Casein Kinase II Phosphorylation Site.

<220>
 <221> TRANSMEM
 <222> 86-103, 60-75
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 144-151
 <223> Tyrosine Kinase Phosphorylation Site.

<400> 8
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His
 1 5 10 15

Leu	Leu	Val	Leu	Ser	Gly	Ala	Trp	Gly	Met	Gln	Met	Trp	Val	Thr	
				20					25					30	
Phe	Val	Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr	
				35					40					45	
Phe	Gly	Leu	Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile	
				50					55					60	
Ser	Met	Gly	Cys	Ala	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln	
				65					70					75	
His	Ala	Trp	Ala	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr	
				80					85					90	
Leu	Leu	Phe	Leu	Ser	Leu	Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp	
				95					100					105	
Leu	Glu	Pro	Arg	Thr	Thr	Ala	Ala	Met	Trp	Ala	Leu	Gln	Thr	Val	
				110					115					120	
Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly	Glu	Val	Pro	Gly	Ser	His	Gln	
				125					130					135	
Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg	Glu	Lys	Asp	Pro	Lys	Tyr	
				140					145					150	
Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr	His	Gly	Leu	Ser	Ser	
				155					160					165	
Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly	Leu	Cys	Leu	Ala	
				170					175					180	
Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu							
				185											

<210> 9
 <211> 1508
 <212> DNA
 <213> Homo sapiens

<400> 9
 aattcagatt ttaagcccat tctgcagtgg aatttcatga actagcaaga 50
 ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100
 agggggaaaa atgctctttt ggggtgctagg cctcctaata ctctgtgggt 150
 ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200
 tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250
 aacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat 300
 caggatcaac agctttaaaag gcagaaacct cagagagact tcgtactgtg 350
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

gaagaaccaa gttggggaga aaggtctctg gggctctgatc aataatgctg 450
 gtgttccccg cgtgctggct cccactgact ggctgacact agaggactac 500
 agagaaccta ttgaagtga cctgtttgga ctcatcagtg tgacactaaa 550
 tatgcttcct ttgggtcaaga aagctcaagg gagagttatt aatgtctcca 600
 gtgttggagg tcgccttgca atcgttggag ggggctatac tccatccaaa 650
 tatgcagtgg aagggtttcaa tgacagctta agacgggaca tgaaagcttt 700
 tgggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750
 cagatccagt aaaggtaatt gaaaaaaaaac tcgccatttg ggagcagctg 800
 tctccagaca tcaaacaaca atatggagaa gggtacattg aaaaaagtct 850
 agacaaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900
 tggtagagtg catggaccac gctctaacaa gtctcttccc taagactcat 950
 tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000
 gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
 ctaatcccaa ggcagtgtga ctgagctaac cacaaatgtc tcctccaggc 1100
 tatgaaattg gccgatttca agaacacatc tccttttcaa cccatttcct 1150
 tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200
 agggagtccc accatcgctg gtggtatccc agggtccttg ctcaagtttt 1250
 ctttgaaaag gagggctgga atggtacatc acataggcaa gtctgcct 1300
 gtatttaggc ttgcctgct tgggtgtgatg taagggaat tgaaagactt 1350
 gccattcaa aatgatcttt accgtggcct gcccattgot tatgggtccc 1400
 agcatttaca gtaacttgat aatgttaagt atcatctctt atctaaatat 1450
 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaa 1508

<210> 10
 <211> 319
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-17
 <223> Signal Peptide

<220>
 <221> misc_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212
 <223> N-myristoylation Sites.

<220>
 <221> misc_feature
 <222> 39-42
 <223> Glycosaminoglycan Attachment Site.

<220>
 <221> TRANSMEM
 <222> 136-152
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 161-163, 187-190 and 253-256
 <223> N-glycosylation Sites.

<400> 10
 Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
 1 5 10 15
 Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
 20 25 30
 Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
 35 40 45
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
 50 55 60
 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
 65 70 75
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
 80 85 90
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
 95 100 105
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
 110 115 120
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
 125 130 135
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
 140 145 150
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
 155 160 165
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
 170 175 180
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
 185 190 195

10045610-121204

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
 agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
 gtgtccagggt ccttcagtga gtgggttggc ctcggtctca cactgatcga 900
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
 aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
 ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
 atcggctaata gcctgccttc agaacacat ccaagattcc ttactcggat 1150
 gtgaacatcg gtactggagt tgcccaccg ccacgggtga cctccgacag 1200
 cactgtggcc gaggtgacca gcattcagct ggagttccg gagctctccc 1250
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
 cacatccacg gcctgtcttg gaagaaggat gggctgggtc ccatgttcat 1350
 caatacccac agtggcctct tcaaacacct gggcgtattc acgctgggag 1400
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
 gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
 tgtcagaacg cacctgtctg ggcactccga gccagtaag ctcacctttg 1550
 tgggggagct tgcccacggc cgcttcagt ccaagatgga ccacctggtg 1600
 tgcttcctgc caggacgct ggctctgggc gtctaccacg gcctgcccgc 1650
 cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750
 tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800
 caacctgctg cggccagaga ccgtggagag cctgtttctac ctgtaccgag 1850
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
 tcctggggga gacgtcaag tatctgttct tgctcttctc cgatgaccca 2050
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aagggccac 2200
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
 ttctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500
 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggctgg ctctggtgtt tacaagctgg actcagggat 2600
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gcccctccag tggaatgggt cttttcgggtg gagataaaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			

395					400					405				
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
				680					685					690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgccctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtcg ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgcct ggcagtgtctg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat ggcgcgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgtctc accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgga gaagcaacag cacggactac 550
 attgccatgc acgaogttga cctgtctcct ctcaacgagg agctggacta 600
 tggttttctt gaggtgggc ccttcacagt ggctccccc gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttccgccc ctccggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
 acaggagcag ttcaaggtgg acaggaggagg aggcctgaac actgtgaagt 950
 accatgtggc ttcccgact gccctgtctg tggggggggc cccctgcact 1000
 gtcctcaaca tcatgttgga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtggggccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200
 ggccgccaag gcaggcttgg gctggggccag gacacgtggg gtgcctggga 1250
 cgctgcttgc catgcacagt gatcagagag aggtgggggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

```

<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1             5             10             15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
          20             25             30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
          35             40             45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
          50             55             60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
          65             70             75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
          80             85             90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
          95             100            105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
          110            115            120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
          125            130            135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

```


<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagtgg gagatagggg acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggctcc ctagaggccc agcgagccg 50
cagcggacaa aggagcatgt ccgcgcggg gaaggcccg cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgtta ggccagtgcg ccgcccgtcg ccccgagccg 200
cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgagc 250
cgccgctgtt gctgcgcgtc tcgctgttag cgctgctgcg gctgctggga 300
ggcggcgggc gcggcgggcg ccggcgctg cccgccggct gcaagcacga 350
tgggcggccc cgaggggctg gcagggcggc gggcgccgcg gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagg tctgcccc agatactctg 450
cccaaccgca cggtcacct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggtg cgggatacca 850

ggtgtgttta tctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggtatth ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaa 1200
 cgtgggaata atacgaggac tgtggatatt gtggtattag agagttctgc 1250
 acagtactgt cctccagaga ggggtgtaaa caacaaagggt gacttcagat 1300
 ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
 gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500
 atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550
 ttacactgtg gaagcagcca acttttctga caaatggat gttatatttg 1600
 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650
 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700
 tgatgaacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
 ggattgtgca gtgtcttcag cgattgcta cctaccggct agccggtgga 1800
 gctcacgttt attcaacata ttcaccaat attgctctgg aagcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950
 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050
 ctattttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat tttataactg cagtgggtata aatgcaaata tactattgtt 2300

acatgtgaaa aaatatttatt tgacttaaaa gtttatttat ttgttttttt 2350
gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
atgagccttt ggcactgcgc ctgccaagcc tagtgagagaa gtcaaccctg 2450
agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
acacaaatat gtcatatatc ttttttttaa aaaagtattt cattgaagca 2550
agcaaatga aagcattttt actgattttt aaaattggtg ctttagatat 2600
atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650
ctaattggaac cacatttttt tcaacttagct ttctgtgggc atgtgtaatt 2700
gtatttctctg cggtttttaa tctcacagta ctttatttct gtcttgcccc 2750
tcaataatat cacaacaat attccagtca ttttaattggc tgcataataa 2800
ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850
tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
1 5 10 15
Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
20 25 30
Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn	Lys	Ile	Ser	Glu 95	Leu	Lys	Asn	Gly	Ser 100	Phe	Ser	Gly	Leu	Ser 105
Leu	Leu	Glu	Arg	Leu 110	Asp	Leu	Arg	Asn	Asn 115	Leu	Ile	Ser	Ser	Ile 120
Asp	Pro	Gly	Ala	Phe 125	Trp	Gly	Leu	Ser	Ser 130	Leu	Lys	Arg	Leu	Asp 135
Leu	Thr	Asn	Asn	Arg 140	Ile	Gly	Cys	Leu	Asn 145	Ala	Asp	Ile	Phe	Arg 150
Gly	Leu	Thr	Asn	Leu 155	Val	Arg	Leu	Asn	Leu 160	Ser	Gly	Asn	Leu	Phe 165
Ser	Ser	Leu	Ser	Gln 170	Gly	Thr	Phe	Asp	Tyr 175	Leu	Ala	Ser	Leu	Arg 180
Ser	Leu	Glu	Phe	Gln 185	Thr	Glu	Tyr	Leu	Leu 190	Cys	Asp	Cys	Asn	Ile 195
Leu	Trp	Met	His	Arg 200	Trp	Val	Lys	Glu	Lys 205	Asn	Ile	Thr	Val	Arg 210
Asp	Thr	Arg	Cys	Val 215	Tyr	Pro	Lys	Ser	Leu 220	Gln	Ala	Gln	Pro	Val 225
Thr	Gly	Val	Lys	Gln 230	Glu	Leu	Leu	Thr	Cys 235	Asp	Pro	Pro	Leu	Glu 240
Leu	Pro	Ser	Phe	Tyr 245	Met	Thr	Pro	Ser	His 250	Arg	Gln	Val	Val	Phe 255
Glu	Gly	Asp	Ser	Leu 260	Pro	Phe	Gln	Cys	Met 265	Ala	Ser	Tyr	Ile	Asp 270
Gln	Asp	Met	Gln	Val 275	Leu	Trp	Tyr	Gln	Asp 280	Gly	Arg	Ile	Val	Glu 285
Thr	Asp	Glu	Ser	Gln 290	Gly	Ile	Phe	Val	Glu 295	Lys	Asn	Met	Ile	His 300
Asn	Cys	Ser	Leu	Ile 305	Ala	Ser	Ala	Leu	Thr 310	Ile	Ser	Asn	Ile	Gln 315
Ala	Gly	Ser	Thr	Gly 320	Asn	Trp	Gly	Cys	His 325	Val	Gln	Thr	Lys	Arg 330
Gly	Asn	Asn	Thr	Arg 335	Thr	Val	Asp	Ile	Val 340	Val	Leu	Glu	Ser	Ser 345
Ala	Gln	Tyr	Cys	Pro 350	Pro	Glu	Arg	Val	Val 355	Asn	Asn	Lys	Gly	Asp 360
Phe	Arg	Trp	Pro	Arg 365	Thr	Leu	Ala	Gly	Ile 370	Thr	Ala	Tyr	Leu	Gln 375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro

	380		385		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcggg 150
aaaaagaaaa cattcgtctt ttgggagAAC agattatctt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttgagca gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500
tgtccagtgc ttaggggtgt tactgagaag cactgccgag cttgtgagaa 550

ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500
atgtccagtt cctgtcccac ggccgttcgc gggaccacgc catcgccgcc 550
accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600
gaccggggcc cggcccggcg agatcactgg ctatatggcc accgtaccgc 650
ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700
atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750
ggcgggtgtac gccatctgct tcctcctagc ggccatcgcc atcctgctga 800
acctggggga gtgcaccaac gtgctacca tccccttccc cagcttcctg 850
tcggggctgg ccttgctgtc tgtcctcctc tatgccaccg cccttgttct 900
ctggccctc taccagttcg atgagaagta tggcggccag cctcggcgct 950
cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000
gaccgccgac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050
tgtggctgac ctgggtgact ctgccacct gggttttgtc aaggtctaag 1100
actctcccaa gaggtcccc ttccctctcc aacctcttg ttcttcttg 1150
ccgagttttc tttatggagt acttctttcc tccgcctttc ctctgttttc 1200
ctcttctgt ctccctccc tcccacctt ttctttcctt cccaattcct 1250
tgactctaa ccagttcttg gatgcattt ctctctccc ttctctcttg 1300
ctgtttcctt cctgtgtgtt tttgttgccc acatcctgtt ttcacccctg 1350
agctgtttct cttttcttt tctttcttt ttttttttt ttttaagacg 1400
gattctcact ctgtggccca ggctggagtg cagtgggtgc atctcagctc 1450
actgcaaccc ccgcctcctg ggttcaagcg attctctcc cccagcctcc 1500
caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550
ttttccactc ttcttttttc tcctctcttt tctgggttgc ctgtcggctt 1600
tcttatctgc ctgttttgca agcaccttct cctgtgtcct tgggagccct 1650
gagacttctt tctctccttg cctccaccca cctccaaagg tgctgagctc 1700
acatccacac cccttgacgc cgtccatgcc acagccccc aaggggcccc 1750
attgccaaag catgcctgcc caccctcgt gtgccttagt cagtgtgtac 1800
gtgtgtgtgt gtgtgtgttt ggggggtggg ggggtggtag ctggggattg 1850
ggcctcttt ctccagtg aggaaggtgt gcagtgtact tcccctttaa 1900

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
 ccactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100
 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr	1	5	10	15
Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	20	25	30	
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	35	40	45	
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	50	55	60	
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	65	70	75	
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	80	85	90	
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	95	100	105	
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	110	115	120	
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	125	130	135	
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	140	145	150	
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	155	160	165	
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	170	175	180	
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	185	190	195	
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr	200	205	210	

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
305 310 315

His Leu Val Phe Val Lys Val
320

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

gaacgtgccca ccatgccag ctaatttttg tatttttagt agagacgggg 50

tttcaccatg ttggccaggc tggctttgaa ctctgtgacct catgatccgc 100

tcacctcggc ctcccaaagt gctgggatta caggcatgag ccaactgacgc 150

ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200

taaacattgg gcactacagt gacaaaaaca gactgaattc cccaagagcc 250

aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300

ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350

tgatttgtaa agagactaca gagggaggac agactaccaa gagggggggcc 400

aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450

gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500

cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550

ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600

aagggaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650

gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750
 tgggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800
 agaaggtgtg ggggttttgt ttccatcttg ccgagtctgc cggaatgtgg 850
 atgggaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900
 agaagtcttg gatgccacac tcttcttctt tctctctctt cctctctctc 950
 agaggtctca ctctgtgttc ttcatcttct gccctgcctc catctctctt 1000
 ggggtgctggg aaagtggagg attagctgaa gttttgcttc tcggggcctg 1050
 tctgaatctc cattgtcttc tgggaggaca taattcacct gtcttagctt 1100
 cttatcatct tacatttccc tgtagccact gggacatatg tgggtgttct 1150
 tcctagctcc tgtctcctcc tcatgccttt gctgggtatg ggcatgttag 1200
 ggggaaggtc attgctgtca gaggggcact gactttctaa tgggtgttacc 1250
 caaggtgaat gttggagaca cagtcgcgat gctgcccaag tcccggcgag 1300
 ccctaactat ccaggagatc gctgcgctgg ccaggtcctc cctgcatggt 1350
 atgcagcccc tcccatgttt ctggccaact tgtectttct cctcccgttt 1400
 gcacatccct ttggaactgt ttctgtgag tacatgctgg ggtctcccct 1450
 ttcttccctt gtcagggtga atctcagccc cttctccac ccaaaggttc 1500
 acatggatcc taactactgc cacccttcca cctccctgca cctgtgctcc 1550
 ctggcctggt cctttaccag gcttctccac cctcccctat ctccaggtat 1600
 ttcccagggt gtgaaggacc acgtgaccaa gcctaccgcc atggcccagg 1650
 gccgagtggc tcacctcatt gagtgggaagg gctggagcaa gccgagtgc 1700
 tcacctgctg ccctggaatc agccttttcc tcctattcag acctcagcga 1750
 gggcgaacaa gaggtctgct ttgcagcagg agtggctgag cagtttgcca 1800
 tcgcggaagc caagctccga gcatggtctt cgggtgatgg cgaggactcc 1850
 actgatgact cctatgatga ggactttgct ggggggaatgg acacagacat 1900
 ggctgggcag ctgcccctgg ggccgcacct ccaggacctg ttcaccggcc 1950
 accggttctc ccggcctgtg cgccagggct ccgtggagcc tgagagcgac 2000
 tgctcacaga ccgtgtcccc agacacctg tgctctagtc tgtgcagcct 2050
 ggaggatggg ttgttgggct ccccgcccg gctggcctcc cagctgctgg 2100
 gcgatgagct gcttctcgcc aaactgcccc ccagccggga aagtgccttc 2150

cgagcctg	gcccactgga	ggcccaggac	tcactctaca	actcgcccct	2200
cacagagtcc	tgcctttccc	ccgcggagga	ggagccagcc	ccctgcaagg	2250
actgccagcc	actctgcccc	ccactaacgg	gcagctggga	acggcagcgg	2300
caagcctctg	acctggcctc	ttctgggggtg	gtgtccttag	atgaggatga	2350
ggcagagcca	gaggaacagt	gaccacatc	atgcctggca	gtggcatgca	2400
tcccccggt	gctgccaggg	gcagagcctc	tgtgcccagg	tgtgggctca	2450
aggctcccag	cagagctcca	cagcctagag	ggctcctggg	agcgctcgct	2500
tctccgttgt	gtgttttgca	tgaaagtgtt	tggagaggag	gcaggggctg	2550
ggctgggggc	gcatgtcctg	ccccactcc	cggggccttg	cgggggttgc	2600
ccggggcctc	tggggcatgg	ctacagctgt	ggcagacagt	gatgttcatg	2650
ttcttaaaat	gccacacaca	catttcctcc	tcggataatg	tgaaccacta	2700
aggggggtgt	gactgggctg	tgtgagggtg	gggtgggagg	ggggccagca	2750
acccccacc	ctcccatg	ctctctcttc	tctgcttttc	ttctcacttc	2800
cgagtccatg	tgcagtgtt	gatagaatca	ccccacctg	gaggggctgg	2850
ctctgccct	ccggagcct	atgggttag	ccgtccctca	agggccctg	2900
cccagctggg	ctcgtgtgt	gcttcattca	cctctccatc	gtctctaaat	2950
cttctctttt	tttcctaaag	acagaagggt	tttggtctgt	tttttcagtc	3000
ggatcttctc	ttctctggga	ggctttggaa	tgatgaaagc	atgtaccctc	3050
cacccttttc	ctggccccct	aatggggcct	gggccctttc	ccaaccctc	3100
ctaggatgtg	cgggcagtgt	gctggcgcct	cacagccagc	cgggctgcc	3150
attcacgcag	agctctctga	gcgggagggtg	gaagaaagga	tggctctggt	3200
tgccacagag	ctgggacttc	atgttcttct	agagagggcc	acaagagggc	3250
cacaggggtg	gccgggagtt	gtcagctgat	gcctgctgag	aggcaggaat	3300
tgtgccagt	agtgacagtc	atgagggagt	gtctcttctt	ggggaggaaa	3350
gaaggtagag	cctttctgtc	tgaatgaaag	gccaaaggcta	cagtacagg	3400
ccccgcccc	gccagggtgt	taatgccac	gtagtggagg	cctctggcag	3450
atcctgcatt	ccaaggtcac	tggactgtac	gtttttatgg	ttgtgggaag	3500
ggtgggtggc	tttagaatta	agggccttgt	aggctttggc	aggtaagagg	3550
gccaaggt	agaacgagag	ccaacgggca	caagcattct	atatataagt	3600

ggctcattag gtgtttatatt tgttctatatt aagaatttgt tttattaaat 3650

taatataaaa atcttttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro	1	5	10	15
Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser	20	25	30	
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val	35	40	45	
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu	50	55	60	
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu	65	70	75	
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro	80	85	90	
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys	95	100	105	
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala	110	115	120	
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	125	130	135	
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys	140	145	150	
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp	155	160	165	
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala	170	175	180	
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly	185	190	195	
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	200	205	210	
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	215	220	225	
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu	230	235	240	

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccacactaa 50

ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100

ccatctgttt tototaatgc acgacagatt cctttcagac aggacaactg 150

tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250

caatctattc ttgccacatc aagggattgt tattccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaccac ctcaaacttc aaggcgagtc attccccctcc tttgaatcta 550
ccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600
gcattctttg ggcagtctaa aaccacacatc taccatttcc acaagccctc 650
ccttgatcca tagctttggt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgcccat ctacgcacat cccaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
ccatctgtga ccccttgat agtggaaacca agtggatggc ttaccacaaa 900
cagtgatagc ttcactgggt ttaccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
aggtgctatt ctgggtgtct cattgcttac tottggtgggc tacttggtgt 1100
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150
agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
tgccagaaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agccttttga caaattcatt tttcaaaagg 1400
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500
tttcttaciaa tttttggcca tctgaggca tttactaagt agccttaatt 1550
tgtattttag tagtattttc ttagtagaaa atatttgtgg aatcagataa 1600
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700
tgctgaagc ctagtagcca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgcttttttaa agaaaatttg acttaaagct aaaaagagga 1800
catagcccag agttttctgtt attgggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agctttctta aaagtcttca 2000
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330
Arg Thr Ser Val														

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgacg tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccga gaggaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct togtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750
ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgactttta cattaagggt tatgggatac 950
tcaagatatt tactcatgca tttactctat tgcttatgct ttaaaaaaag 1000
gaaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttggttt ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300
tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
aatgcagtga ttcttttca ctactatctg tattgtggaa tgcacaaaat 1500
tgtgtagggt ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
1				5					10					15
Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30
Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45
Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu

<211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 45
 gggaactgct atctgatgcc 20

<210> 46
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 46
 caggatctcc tcttcagtc tgcagc 26

<210> 47
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 48
 cagattccc tccacagcaa ctggg 25

<210> 49
 <211> 1969
 <212> DNA
 <213> Homo sapiens

<400> 49
 ggaggaggga gggcgggcag ggcagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccagggtgcc cccactctcg ctccattcgg 100
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150
 gtttcggcgg cagccccag cctcctcatc cttctgttgc tgetgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
 ccgagcctcc cgccaccctg gaccccggcc ctacgcccc catcgatggg 350
 gccccagccc acaaccctgg gggggccatc accccccacc aacttcctgg 400
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgetgtggtg 450
 ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcacac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc tcccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccttgattc 650
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtcaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
 tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
 agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050
 ccccggtgat gaaaaggcct tcagccctga ctgcttctg aactccctc 1100
 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
 cagaaatgct ggtccccgtt gccccggagg aatcttacca agtgccatca 1200
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgctc ttaattttcc tgaagggtgg cccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacc ccgacctggg gtgagtttct catcccgtc ctgctgctgg 1550
gatcagggtg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
agaagctgag gggctgtgtt tgaggggacc tccacctgg ggaagtccga 1650
ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
ccacccctg ttgtcacac attgtctggc agcctgtgtc cacaatattc 1750
gtcagtcctc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800
ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccagggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
aaaaaaaaa aaaaaaaga 1969

<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu
				20					25					30
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu
				35					40					45
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro
				50					55					60
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly
				65					70					75
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe
				80					85					90
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala
				95					100					105
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln
				110					115					120
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys
				125					130					135
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe
				140					145					150
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala
				155					160					165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
				260					265					270	
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
				275					280						

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggcag ctggctctaa agtcagtgag gcccttggcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
 ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaaggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtogg gcagcagtgg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaaccgg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15

Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30

Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45

Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

				50						55					60
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr	
				65					70					75	
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly	
				80					85					90	
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala	
				95					100					105	
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val	
				110					115					120	
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val	
				125					130					135	
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile	
				140					145					150	
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro	
				155					160					165	
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser	
				170					175					180	
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln	
				185					190					195	
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly	
				200					205					210	
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln	
				215					220					225	
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly	
				230					235					240	
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	
				245					250					255	
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly	
				260					265					270	
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	
				275					280					285	
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser	
				290					295					300	
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly	
				305					310					315	
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His	
				320					325					330	
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	
				335					340					345	

gagttctgtc aaaggaagag ccctggggct gtgcggggcg tgcttccaga 850
 ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
 ttgcaacaga gaaagcctgt gcttggtgtg cagccaacat cacagcactg 950
 atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
 tcctgaacct gctgcccggg gggagcggag gggctgctcc cgcgccctgac 1050
 gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100
 agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
 gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgtg 1200
 gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggccccc 1250
 ggcacagtac aggctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300
 tgctttcctt gtggaaggaa gactttcagg ggccggttcc gctgcagctg 1350
 ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400
 gtgggacttg ctgctattct tgctacggga gctgggtggag aagggtctga 1450
 tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500
 tggccagggg actttgctga agaattagca aactgtcta atctgtttct 1550
 agccgagccc cacctgccag aaccccagct aagagcctgt gagttggtgc 1600
 agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650
 ctgccttggg cattgcacca gaaccctgga ccccgccctc acgaggaggc 1700
 ccaagtgcc aatgcagacc ctactgggtt ggggtgtagc tgggtctaca 1750
 gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgcga 1800
 atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850
 cagagatgcc agtcctggag tagaagaggt ggtgtttggt tatctcttgg 1900
 atactaaatg aaatgaggtg tgtgggcttg tcaacacaga attcaagcct 1950
 catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000
 cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
 cttgggagtc tacatthttct tatcaccagg agctggactg ccatctcctt 2100
 ataaatgcct aacacaggcc gggctctggtg gctcatgcct gtaatcccag 2150
 cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200
 accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

tatttagctg	ggcatgggtg	tgtgtgcctg	taatcccagc	tactcaggag	2300
gatgaggcag	gagacctgct	tgaacctgga	ggtggagggt	gcagtgagcc	2350
gaggtcgcac	cactgcactc	cagtctgggt	aacagagcga	gactttctag	2400
aaaaagccta	acaaacagat	aaggtaggac	tcaaccaact	gaaacctgac	2450
tttccccctg	taccttcage	ccctgtgcag	gtagtaacct	cttgagacct	2500
ctccctgacc	agggaccaag	cacagggcac	ttagagcttt	ttagaataaa	2550
ctggttttct	ttaaaaaaaaa	aaaaaaaaaa	agggcggccg	cccttttttt	2600
tttttttttt	tttttttttt	tttttttttt	tttttttttt	taaaaagggc	2650
ttttattaaa	attctcccca	cacgatggct	cctgcaatct	gccacagctc	2700
tggggcgtgt	cctgtaggga	aaggccctgt	tttccctgag	gcggggctgg	2750
gcttgtccat	gggtccgcgg	agctggccgt	gcttggcgcc	ctggcgtgtg	2800
tctagctgct	tcttgccggg	cacagagctg	cggggtcttg	gggcaccggg	2850
agctaagagc	aggctctggt	gcaggggttg	aggcctgtct	cttaaccgac	2900
accctgaggt	gctoctgaga	tgctgggtcc	accctgagtg	gcacggggag	2950
cagctgtggc	cggtgctcct	tcytaggcca	gtcctgggga	aactaagctc	3000
gggcccttct	ttgcaaagac	cgaggatggg	gtgggtgttg	gggactcatg	3050
gggaatggcc	tgaggagcta	cgtgtgaaga	gggcgcgggt	ttgttggttg	3100
cagcggcctg	gagcgcctct	ctcctgagcc	tcagtttccc	tttcggtcta	3150
atgaagaaca	tgccgtctcg	gtgtctcagg	gctattagga	cttgccctca	3200
ggaagtggcc	ttggacgagc	gtcatgttat	tttcacaact	gtcctgcgac	3250
gttggccttg	gcacgtcatg	gaatggccca	tgtccctctg	ctgcgtggac	3300
gtcgcggtcg	ggagtgcgca	gccagaggcg	gggccagacg	tgcgccctgg	3350
ggtgagggga	ggcgccccgg	gagggcctca	caggaagttg	ggctcccgca	3400
ccaccaggca	ggggggggctc	ccgccgccgc	cgccgccacc	accgtccagg	3450
ggccggtaga	caaagtggaa	gtcgcgcttg	ggctcgctgc	gcagcaggta	3500
gcccttgatg	cagtgcggca	gcgcgtcgtc	cgccagctgg	aagcagcgcc	3550
cgccaccag	cacgaacagc	cgggtgcgcct	3580		

<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

Met	Cys	Phe	Leu	Asn	Lys	Leu	Leu	Leu	Leu	Ala	Val	Leu	Gly	Trp
1				5					10					15
Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
				275					280					

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
tcccttgaca ggtctggtgg ctggttcggg gtctactgaa ggctgtcttg 50
atcaggaaac tgaagactct ctgcttttgc cacagcagtt cctgcagctt 100
ccttgagggtg tgaaccaca tccctgcccc cagggccacc tgcaggacgc 150
cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
gcagcgggtca gcagtgttcg tgatcctctt tgccctcatc accatcctca 250
tcctctacag ctccaacagt gccaatgagg tcttccatta cggctccctg 300
cggggccgta gccgccgacc tgtcaacctc aagaagtgga gcatcactga 350
cggctatgtc ccattctcgc gcaacaagac actgccctct cggtgccacc 400
agtgtgtgat tgtcagcagc tccagccacc tgctgggcac caagctgggc 450
cctgagatcg agcgggctga gtgtacaatc cgcataatg atgcaccac 500
cactggctac tcagctgatg tgggcaacaa gaccacctac cgcgtcgtgg 550
ccattccag tgtgttccgc gtgctgagga ggccccagga gtttgtcaac 600
cggacccctg aaaccgtgtt catcttctgg gggccccga gcaagatgca 650
gaagccccag ggcagcctcg tgcgtgtgat ccagcgagcg ggcctggtgt 700
tccccaacat ggaagcatat gccgtctctc cgggccgcat gcggcaattt 750
gacgacctct tccggggtga gacgggcaag gacagggaga agtctcattc 800
gtggttgagc acaggctggt ttaccatggt gatcgcggtg gagttgtgtg 850
accacgtgca tgtctatggc atgggtcccc ccaactactg cagccagcgg 900
ccccgcctcc agcgcagtgc ctaccactac tacgagcca aggggccgga 950
cgaatgtgtc acctacatcc agaatgagca cagtcgcaag ggcaaccacc 1000
accgcttcat caccgagaaa agggctcttct catcgtgggc ccagctgtat 1050
ggcatcacct tctcccaccc ctcttgacc taggccaccc agcctgtggg 1100
acctcaggag ggtcagagga gaagcagcct ccgccagcc gctaggccag 1150
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaatc 1200
agggccttga ggaggatgta tcctccagcc aatcagggcc tggggaatct 1250
gttggcgaat cagggatttg ggagtctatg tggttaatca ggggtgtctt 1300

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg	
				35					40					45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	
				50					55					60	
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val	
				65					70					75	
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	
				80					85					90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
				95					100					105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
				110					115					120	
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	
				125					130					135	
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly	
				140					145					150	
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	
				155					160					165	
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala	
				170					175					180	
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly	
				185					190					195	
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr	
				200					205					210	
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val	
				215					220					225	
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro	
				230					235					240	
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
				245					250					255	
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly	
				260					265					270	
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp	
				275					280					285	
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr		
				290					295						

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

tctcccgag ggcctgagc gtgctcagca tggggcctga ggacgaaggc 1500
gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550
ccagctgogg acctccaggc caagcataac cccaaggcta tggcaggatg 1600
ctgagctggc tactggcaca cctcctgtat caccctccaa actcggcaac 1650
cctgagcaga tgctgagggg gcaaccggcg ctccccagac cccaacgctc 1700
agtggggcct gcttccccga agtgtccagg agagaagggg cagggggctc 1750
ccgccgaggc toccatcatc ctgagctcgc cccgcacctc caagacagac 1800
tcatatgaac tgggtgtggcg gcctcggcat gagggcagtg gccgggagcc 1850
aatcctctac tatgtggtga aacaccgcaa gcaggtcaca aattcctctg 1900
acgattggac catctctggc attccagcca accagcaccg cctgaccctc 1950
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacia 2000
ctgtgcggga gagggccaga cagccatggt caccttccga actggacggc 2050
ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100
gaccctggag ccagtcccca gagcagcagc cagccagacc acggccgcct 2150
ctcccccca gaagctcccg acaggccac catctccacg gcctccgaga 2200
cctcagtgtg cgtgacctgg attccccgtg ggaatggtgg gttcccaatc 2250
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300
tctggccacc agcgccatcc ccccatcgcg gctgtccgtg gagatcacgg 2350
gcctagagaa aggcacctcc tacaagtttc gagtccgggc tctgaacatg 2400
ctggggggaga gcgagcccag cggccctctc cggccctacg tgggtgtcggg 2450
ctacagcggg cgcgtgtacg agaggcccg ggcaggtcct tatatcacct 2500
tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550
ccagcaagta acaacaacac cccaatccat ggcttttata tctattatcg 2600
accacagac agtgacaatg atagtgacta caagaaggat atggtggaag 2650
gggacaagta ctggcactcc atcagccacc tgcagccaga gacctcctac 2700
gacattaaga tgcaagtgtt caatgaagga ggggagagcg agttcagcaa 2750
cgtgatgatc tgtgagacca aagctcgaa gtcttctggc cagcctggctc 2800
gactgccacc cccaactctg gccccaccac agccgcccct tcctgaaacc 2850
atagagcggc cgggtgggcac tggggccatg gtggctcgct ccagcgacct 2900

gccctatctg attgtcgggg tcgtcctggg ctccatcggt ctcacatcgc 2950
 tcaccttcat ccccttctgc ttgtggaggg cctgggtctaa gcaaaaaacat 3000
 acaacagacc tgggttttcc tcgaagtgcc cttccaccct cctgcccgta 3050
 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
 cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150
 aataggggct gcccctcggc tgcagtgggc taccggggca tgaagcccca 3200
 gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250
 tgaggcagac ccattctggc aatggatatg acccccaaag tcaccagatc 3300
 acgagggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350
 gcccgacgac tccactcacc agctgctgca gcccacacac gactgctgcc 3400
 aacgccagga gcagcctgct gctgtggggc agtcaggggt gaggagagcc 3450
 cccgacagtc ctgtcctgga agcagtgtgg gaccctccat ttcactcagg 3500
 gcccccatgc tgcttggggc ttgtgccagt tgaagagggt gacagtcctg 3550
 actcctgcca agtgagtgga ggagactggt gtccccagca ccccgtaggg 3600
 gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650
 gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700
 tcccagaaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattggta tttatttttc tattatagcc atatttata 3800
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850
 taaggagtcc taccggttga ggttggagag ggaaaataaa gaagctgcca 3900
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050
 tgagggaaca gcaaggggca cggtatcaca gcctggagac acccacacag 4100
 atggctggat ccggtgctac gggaaacatt ttctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58

<211> 1115

<212> PRT
 <213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu		1	5	10	15
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala		20	25	30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr		35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu		50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu		65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr		80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln		95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala		110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln		125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys		140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val		155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met		170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu		185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val		200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr		215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile		230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser		245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser		260	265	270	

Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu	275	280	285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met	290	295	300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr	305	310	315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser	320	325	330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu	335	340	345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala	350	355	360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala	365	370	375
Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg			

	560		565		570
Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile	Gln		
	575	580	585		
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro	Asp		
	590	595	600		
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr	Ile		
	605	610	615		
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro	Arg		
	620	625	630		
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr	Lys		
	635	640	645		
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala	Ile		
	650	655	660		
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys	Gly		
	665	670	675		
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly	Glu		
	680	685	690		
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly	Tyr		
	695	700	705		
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile	Thr		
	710	715	720		
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp	Met		
	725	730	735		
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe	Tyr		
	740	745	750		
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr	Lys		
	755	760	765		
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser	His		
	770	775	780		
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe	Asn		
	785	790	795		
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu	Thr		
	800	805	810		
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro	Pro		
	815	820	825		
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu	Arg		
	830	835	840		
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu	Pro		
	845	850	855		

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

				260					265					270
Ser	Asp	Thr	Leu	Ile 275	Arg	Arg	Val	Leu	Glu 280	Val	Ser	Gln	Ala	Pro 285
Val	Ile	Phe	Ser	His 290	Ser	Ala	Ala	Arg	Ala 295	Val	Cys	Asp	Asn	Leu 300
Leu	Asn	Val	Pro	Asp 305	Asp	Ile	Leu	Gln	Leu 310	Leu	Lys	Asn	Gly	Gly 315
Ile	Val	Met	Val	Thr 320	Leu	Ser	Met	Gly	Val 325	Leu	Gln	Cys	Asn	Leu 330
Leu	Ala	Asn	Val	Ser 335	Thr	Val	Ala	Asp	His 340	Phe	Asp	His	Ile	Arg 345
Ala	Val	Ile	Gly	Ser 350	Glu	Phe	Ile	Gly	Ile 355	Gly	Gly	Asn	Tyr	Asp 360
Gly	Thr	Gly	Arg	Phe 365	Pro	Gln	Gly	Leu	Glu 370	Asp	Val	Ser	Thr	Tyr 375
Pro	Val	Leu	Ile	Glu 380	Glu	Leu	Leu	Ser	Arg 385	Xaa	Trp	Ser	Glu	Glu 390
Glu	Leu	Gln	Gly	Val 395	Leu	Arg	Gly	Asn	Leu 400	Leu	Arg	Val	Phe	Arg 405
Gln	Val	Glu	Lys	Val 410	Arg	Glu	Glu	Ser	Arg 415	Ala	Gln	Ser	Pro	Val 420
Glu	Ala	Glu	Phe	Pro 425	Tyr	Gly	Gln	Leu	Ser 430	Thr	Ser	Cys	His	Ser 435
His	Leu	Val	Pro	Gln 440	Asn	Gly	His	Gln	Ala 445	Thr	His	Leu	Glu	Val 450
Thr	Lys	Gln	Pro	Thr 455	Asn	Arg	Val	Pro	Trp 460	Arg	Ser	Ser	Asn	Ala 465
Ser	Pro	Tyr	Leu	Val 470	Pro	Gly	Leu	Val	Ala 475	Ala	Ala	Thr	Ile	Pro 480
Thr	Phe	Thr	Gln	Trp 485	Leu	Cys								

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
ctccttctcc ctaactttag aaatgttgta cttggtatt ttgattaggg 850
aagagggatg tgggtctctga tctctgttggt cttcttgggt ctttgggggt 900
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
cagctctgag tcttggaat gttgttacct ttggaagata aagctgggtc 1050
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
gttcctttct gcagtggttc ttatcaccac ctccctcca gccccggcgc 1150
ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200
tgggccccct gagccactg ggtcttcagg gtgcactgga agctggtgtt 1250
cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
ctctgctgcc ggtcccctca cctgcacttg aggggtctgg gcagtccctc 1350
ctctccccag tgtccacagt cactgagcca gacggctcgg ttggaacatga 1400
gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450
gcctcttgtc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500
tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
ttttatttct ctca 1564

<210> 68

<211> 183

<212> PRT

<213> Homo sapiens

<400> 68

Met	Lys	Leu	Leu	Ser	Leu	Val	Ala	Val	Val	Gly	Cys	Leu	Leu	Val
1				5					10					15

Pro	Pro	Ala	Glu	Ala	Asn	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Cys	Lys
				20					25					30

Cys	Ile	Cys	Pro	Pro	Tyr	Arg	Asn	Ile	Ser	Gly	His	Ile	Tyr	Asn
				35					40					45

Gln	Asn	Val	Ser	Gln	Lys	Asp	Cys	Asn	Cys	Leu	His	Val	Val	Glu
				50					55					60

cagagatcga	aaccacggtc	attactcaaa	ccatgacttg	ggatggcaga	700
atctaggaag	accacacact	aagatgtcac	atataaaaagg	gcatgaagga	750
gacccctgcc	tacgatcatc	agactgcatt	gaaggggtttt	gctgtgctcg	800
tcattttctgg	accaaaatct	gcaaaccagt	gctccatcag	ggggaagtct	850
gtaccaaaca	acgcaagaag	ggttctcatg	ggctggaaat	tttccagcgt	900
tgcgactgtg	cgaagggcct	gtcttgcaaa	gtatggaaag	atgccaccta	950
ctcctccaaa	gccagactcc	atgtgtgtca	gaaaatttga	tcaccattga	1000
ggaacatcat	caattgcaga	ctgtgaagtt	gtgtatttaa	tgcattatag	1050
catggtggaa	aataaggttc	agatgcagaa	gaatggctaa	aataagaaac	1100
gtgataagaa	tatagatgat	cacaaaaagg	gagaaagaaa	acatgaactg	1150
aatagattag	aatgggtgac	aaatgcagtg	cagccagtg	ttcattatg	1200
caacttgtct	atgtaaataa	tgtacacatt	tgtggaaaat	gctattatta	1250
agagaacaag	cacacagtgg	aaattactga	tgagtagcat	gtgactttcc	1300
aagagtttag	gttgtgctgg	aggagaggtt	tccttcagat	tgctgattgc	1350
ttatacaaat	aacctacatg	ccagatttct	attcaacg	agagttaaac	1400
aaaatactcc	tagaataact	tgttatacaa	taggtttctaa	aaataaaaatt	1450
gctaacaacg	aaatgaaaac	atggagcatt	gttaattttac	aacagaaaat	1500
taccttttga	tttgtaacac	tacttctgct	gttcaatcaa	gagtcottgg	1550
agataagaaa	aaaatcagtc	aatattttcca	aataattgca	aaataatggc	1600
cagttgttta	ggaaggcctt	taggaagaca	aataaataac	aaacaaacag	1650
ccacaaatac	tttttttttca	aaatttttagt	tttacctgta	attaataaga	1700
actgatacaa	gacaaaaaaca	gttccttcag	attctacgga	atgacagtat	1750
atctctcttt	atcctatgtg	attcctgctc	tgaatgcatt	atattttcca	1800
aactataccc	ataaattgtg	actagtaaaa	tacttacaca	gagcagaatt	1850
ttcacagatg	gcaaaaaaat	ttaaagatgt	ccaatatatg	tgggaaaaga	1900
gtaacagag	agatcattat	ttcttaaaga	ttggccataa	cctatatattt	1950
gatagaatta	gattggtaaa	tacatgtatt	catacatact	ctgtggtaat	2000
agagacttaa	gctggatctg	tactgcactg	gagtaagcaa	gaaaattggg	2050
aaaacttttt	cgtttgtttca	ggtttttggca	acacatagat	catatgtctg	2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150
tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250
tgctgagatc ctcaaataat ctcaatttca ggagggttca caaatgtac 2300
tcctgaagta gacagagtag tgagggttca ttgccctcta taagcttctg 2350
actagccaat ggcacatcc aattttcttc ccaaacctct gcagcatctg 2400
ctttattgcc aaagggctag tttcggtttt ctgcagccat tgcgggttaa 2450
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550
aactcagttc taaatacttt gtctggagca caaaacaata aaagggttatc 2600
ttatagtcgt gactttaaac tttttagtag cacaattcac tttttagttt 2650
tcttttactt aaatcccatc tgcagtctca aattttaagtt ctcccagtag 2700
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950
gtccaccctt ttaaaaatta ttatttgaag taatttatat acaggaaatg 3000
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
1				5					10					15
Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250
 atatatttagt aattcatatg ttttagatta taggttttaa cataacttgtg 300
 aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
 ggatttggtc ttttatcccc cttttaaagt catcogtcc tggctcagga 400
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
 ctcaagcccc caacatccca gtccctcagtc ctccagtcac ttgacttcaa 600
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
 agcaccagag ccaggcagtc actgttcctc ctccctgggtt ggagtccttt 700
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
 atacccccag cttctaagat cccagcttct gcagtggaat tgccctggtt 900
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
 aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
 ccgtcattac ctccctgcagt ctgacaagct catcactgaa ttctgctagt 1150
 ccagtagcaa tgtcttctc ttatgaccag agttctgtgc ataacaggat 1200
 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
 tgaatggaca tgggtggtgt cgaagtcagc agacactaga cagtaagtat 1300
 agcagcaagc tactcttgtc atggctggtg ccaaccaaag agaggaagag 1350
 gatagctcac gtgatgtgga aaacaccagt tgggtcaatg ctcatcgtt 1400
 aaaaagcagc ccttttgcct ttttgttttt ggaccaggtg ttggctgtgg 1450
 tgttattaga aatgtcttaa ccacagcaag aaggaggtgg tggctcata 1500
 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
 tttaaagatg cttgggccag gcgggggtggc tgatgcccat aatcccagtg 1600
 ctttggggggg ccaaggcagg cagattgcc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
1 5 10 15
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

<212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct

<400> 75
 ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76
 gccgagtggg acaaagcctg gggctgggcg gggggccatgg cgctgccatc 50
 ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
 tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
 caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
 caccgacggc ccccccggcca ccccccgccta ctgggacggc gagaaggagg 250
 tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
 gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350
 ctgggacggc cagccgcccg gggccccgca cgaccgcgcg gaccgcctgc 400
 tggacctcta cgcgtcgggc gaggcgcgcg cctacgggcc cttttttctg 450
 cgcgaccgcg tggtgtggg cgcggatgcc tttgagcgcg gtgacttctc 500
 actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550
 acctgcacca ccattactgt ggctgcacg aacgccgcgt cttccacctg 600
 acggtcgccc aacccccacg ggagccgccc ccccggggct ctccgggcaa 650
 cggctccagc cacagcggcg cccaggccc agacccaca ctggcgcgcg 700
 gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750
 cagcagctgg gctacgtgct ggccacgctg ctgctcttca tctgtctact 800
 ggtcactgtc ctcttgccg cccgcaggcg ccgcggaggc tacgaatact 850
 cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900
 ttgcgtgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950
 gctagattac aaaaacaaca tctgaagga gagggcggag ctggcccaca 1000
 gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaa at agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
tctcctgtct gtgctcctcg gggcatctcc tgatgctcog gggctcacc 1150
cccttcacgc ggctgggtccc gctttcctgg aatttggcct gggcgtatgc 1200
agaggccgcc tccacacccc tccccagg gcttggtggc agcatagccc 1250
ccaccctgc ggcctttgct cacgggtggc cctgccacc cctggcaca 1300
ccaaaatccc actgatgcc atcatgcct cagacccttc tgggctctgc 1350
ccgctggggg cctgaagaca ttctggagg aactcccat cagaacctgg 1400
cagcccaaaa actggggtca gcctcagggc aggagtcca ctctccagg 1450
gctctgctcg tccggggctg ggagatgttc ctggaggagg aactcccat 1500
cagaacttgg cagccttgaa gttggggtca gcctcggcag gactccact 1550
cctcctgggg tgctgcctgc caccaagagc tccccacct gtaccacct 1600
gtgggactcc aggcaccatc tgtttcccc agggacctgc tgacttgaat 1650
gccagccctt gctcctctgt gttgctttgg gccacctggg gctgcacccc 1700
ctgccctttc tctgccccat cctacccta gccttgctct cagccacctt 1750
gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800
actctgcctg ggctggagtc tagggctggg gctacatttg gcttctgtac 1850
tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900
ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
1				5					10					15
Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala	Arg	Gly	Ala	Pro 80	Ala	Leu	Leu	Thr	Cys 85	Val	Asn	Arg	Gly	His 90
Val	Trp	Thr	Asp	Arg 95	His	Val	Glu	Glu	Ala 100	Gln	Gln	Val	Val	His 105
Trp	Asp	Arg	Gln	Pro 110	Pro	Gly	Val	Pro	His 115	Asp	Arg	Ala	Asp	Arg 120
Leu	Leu	Asp	Leu	Tyr 125	Ala	Ser	Gly	Glu	Arg 130	Arg	Ala	Tyr	Gly	Pro 135
Leu	Phe	Leu	Arg	Asp 140	Arg	Val	Ala	Val	Gly 145	Ala	Asp	Ala	Phe	Glu 150
Arg	Gly	Asp	Phe	Ser 155	Leu	Arg	Ile	Glu	Pro 160	Leu	Glu	Val	Ala	Asp 165
Glu	Gly	Thr	Tyr	Ser 170	Cys	His	Leu	His	His 175	His	Tyr	Cys	Gly	Leu 180
His	Glu	Arg	Arg	Val 185	Phe	His	Leu	Thr	Val 190	Ala	Glu	Pro	His	Ala 195
Glu	Pro	Pro	Pro	Arg 200	Gly	Ser	Pro	Gly	Asn 205	Gly	Ser	Ser	His	Ser 210
Gly	Ala	Pro	Gly	Pro 215	Asp	Pro	Thr	Leu	Ala 220	Arg	Gly	His	Asn	Val 225
Ile	Asn	Val	Ile	Val 230	Pro	Glu	Ser	Arg	Ala 235	His	Phe	Phe	Gln	Gln 240
Leu	Gly	Tyr	Val	Leu 245	Ala	Thr	Leu	Leu	Leu 250	Phe	Ile	Leu	Leu	Leu 255
Val	Thr	Val	Leu	Leu 260	Ala	Ala	Arg	Arg	Arg 265	Arg	Gly	Gly	Tyr	Glu 270
Tyr	Ser	Asp	Gln	Lys 275	Ser	Gly	Lys	Ser	Lys 280	Gly	Lys	Asp	Val	Asn 285
Leu	Ala	Glu	Phe	Ala 290	Val	Ala	Ala	Gly	Asp 295	Gln	Met	Leu	Tyr	Arg 300
Ser	Glu	Asp	Ile	Gln 305	Leu	Asp	Tyr	Lys	Asn 310	Asn	Ile	Leu	Lys	Glu 315
Arg	Ala	Glu	Leu	Ala 320	His	Ser	Pro	Leu	Pro 325	Ala	Lys	Tyr	Ile	Asp 330
Leu	Asp	Lys	Gly	Phe 335	Arg	Lys	Glu	Asn	Cys 340	Lys				

<213> Homo sapiens

gcacctcatc tagaaggagg gacacaagga cattggtgct tcagagcctt 1500
tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaaggcc 1550
taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650
ttccagtcac attaacagaa cactcctgag acagttgaag aagaaatagc 1700
acaaatcagg ggtactccct tcacagctga tggttaacat tccaccttct 1750
ttctagccct tcaaagatgc tgccagtgtt cgccctagag ttattacaaa 1800
gccagtacca aaaccagacc atgggctctt tgcaacctcc cagctgcgct 1850
cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900
gaaggggtct ccctggaatg gaagtccctt ggcatggtca gtcctcaggc 1950
ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000
ccactaacca gactggaaaa ccagaaaga tgggccttcc atgaatgctt 2050
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100
ggcctgggtt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150
cctgggtcaa gatgagggtc tttcagtgtt cctgtttaca acatgtcaaa 2200
gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
1				5					10					15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
			20						25					30
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
			35						40					45
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
			50						55					60
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
			65						70					75
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
			80						85					90
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
			95						100					105

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser		
	410	415	420		
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu	Leu		
	425	430	435		
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly		
	440	445	450		
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly	Ser		
	455	460	465		
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 80

ttttgcggtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 81

cgtagtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-49

<223> Synthetic construct.

<400> 82

tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83

<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100
tcctcgctct cgtccccatc ctctcagcc tggcggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300
gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
taacaggatc gggggccgca tcttcacctc ccgggaccag aacacgggct 400
ggattgggga gctgggagcc atgcgcacgc ccagctctca caggatcctc 450
cacaagctct gccaggcctt ggggctcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
tggcggagaa ggtgcccag aagctgggct acgccttgcg tcccaggaa 600
aagggccact cgcccgaaga catctaccag atggctctca accaggccct 650
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700
ggcacacgct cttggaatat cttctcgggg aggggaacct gagccggccg 750
gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800
cagcttcgcc gaggccctcc gggcccacag ctgcctcagc gacagactcc 850
agtacagccg catcgtgggt ggctgggacc tgctgccgag cgcgctgctg 900
agctcgctgt ccgggcttgt gctgttgaa ggcgccgtgg tggcgatgac 950
ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050
ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttctaa 1150
gcttcgcgag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200
aacaccgatc gcccgctcgc catgattttc taccgcccgc cgcgcgaggg 1250
cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgcttcg 1300
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350

gcattgcacg ggctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400
 caagcgttgg gcggaggacc agcacagcca ggggtggcttt gtggtacagc 1450
 cgccggcgct ctggcaaacg gaaaaggatg actggacggt cccttatggc 1500
 cgcatctact ttgccggcga gcacaccgcc taccgcacg gctgggtgga 1550
 gacggcggtc aagtcggcgc tgcgcgcgc catcaagatc aacagccgga 1600
 aggggcctgc atcgacacg gccagccccg aggggcacgc atctgacatg 1650
 gaggggcagg ggcatgtgca tggggtggcc agcagcccct cgcacacatc 1700
 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	1	5	10	15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	20	25	30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	35	40	45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	50	55	60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	65	70	75	
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	80	85	90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	95	100	105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	110	115	120	
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	125	130	135	
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	140	145	150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	155	160	165	

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro	Glu
170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu	Lys
185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His	Thr
200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro	Ala
215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe	Tyr
230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser	Asp
245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu	Pro
260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn	Ala
275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val	Gln
290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys	Ala
305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg	Ile
320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu	Arg
335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe	Arg
350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser	Asn
365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg	Glu
380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala	Ala
395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala	Leu
410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu	Trp
425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His	Ser
440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr	Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
 ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50
 ctctggggccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcggg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgcga gggctctgaat ttctgtctgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgtc 500
 tgtctgacaa tgggccctgc ttgggatata gaaaacaaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttg cataaaggtt ataaatcatc accagaccag tttgtcggca 650
 tctttgctca gaataggcca gagggatca tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
caccceaaaa ggcattggtg ctgataggga atgtagagaa aggcttcacc 850
ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtggg accacaggtg accceaaagg 1050
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100
aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150
tacctccctc tggctcatat gtttgagagg attgtacagg ctgttggtga 1200
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250
ctgacgacat gaagactttg aagccacat tgtttcccg cgtgcctcga 1300
ctccttaaca ggatctacga taaggtaaa aatgaggcca agacaccctt 1350
gaagaagttc ttgttggaagc tggctgtttc cagtaaattc aaagagcttc 1400
aaaagggtat catcaggcat gatagtttct gggacaagct catctttgca 1450
aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500
tgcccccatg tccacttcag tcatgacatt ctccgggca gcaatgggat 1550
gtcagggtga tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600
tttacattac ctggggactg gacatcaggc cacgttgggg tgcccctggc 1650
ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700
tgaataatga aggagaggtc tgcatcaagg gtacaaacgt gttcaaagga 1750
tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800
gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850
tcatcgaccg taaaaagaac attttcaagc tggccaagg agaatacatt 1900
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
aatttttgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000
ttcctgacac agatgtactt ccctcatttg cagccaagct tggggtgaag 2050
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100
agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150
aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	320	325	330
335		340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu	605	610	615

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700
 ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750
 gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800
 acattctaag tcacctgccc tctcttcctg gggggacca gtctgctga 850
 agacagatgt gccattgagc tcagcagaag aggcagagt ccaactgggca 900
 gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950
 ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
 ctgacctact ccagacaac aaggtcctca atgtgcctgt ggctgtcatt 1050
 gcagggaacc gacccaatta cctgtacagg atgctgcgct ctctgctttc 1100
 agcccagggg gtgtctcctc agatgataac agttttcatt gacggctact 1150
 atgaggaacc catggatgtg gtggcactgt ttggctctgag gggcatccag 1200
 catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250
 cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300
 ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350
 caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
 ctggaatgac caggggtatg aacacacggc tgaggacca gactactgt 1450
 accgtgtgga gaccatgcct gggctgggct gggtgctcag gaggtccttg 1500
 tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550
 ttgggacatg tggatgcgga tgcctgaaca acgccggggc cgagagtgca 1600
 tcatccctga cgtttccga tcctaccact ttggcatcgt cggcctcaac 1650
 atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700
 ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750
 atgaagtgga agttcacagg ctgctcagtg aggctgaggt tctggaccac 1800
 agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850
 ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900
 ccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950
 catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000
 ggggggtccc gcttccccct actcagtga gaagccaccc tcagtcaccc 2050
 caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150
 cccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200
 tggtaggggc tggggctacc ttgtttttta catgagactt aattactaac 2250
 tccaagggga gggttccct gctccaacac cccgttcctg agttaaaagt 2300
 ctatttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350
 attacgatcc ctagcagctc atcctgcctt ttgaataccc tcaactttcca 2400
 ggcctggctc agaatctaac ctatttattg actgtcctga gggccttgaa 2450
 aacaggccga acctggaggg cctggatttc tttttgggct ggaatgctgc 2500
 cctgaggggtg gggctggctc ttactcagga aactgctgtg occaaccat 2550
 ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600
 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
 caaagctgga taagtgtgctc attgattaaa aaaggagaag ccctctggga 2700
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met	Asp	Asp	Trp	Lys	Pro	Ser	Pro	Leu	Ile	Lys	Pro	Phe	Gly	Ala	
1				5					10					15	
Arg	Lys	Lys	Arg	Ser	Trp	Tyr	Leu	Thr	Trp	Lys	Tyr	Lys	Leu	Thr	
				20					25					30	
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu	
				35					40					45	
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp	
				50					55					60	
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu	
				65					70					75	
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg	
				80					85					90	
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser	
				95					100					105	
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu	
				110					115					120	
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val	
				125					130					135	

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

				425					430					435
Asp	Pro	Ala	Leu	Leu 440	Tyr	Arg	Val	Glu	Thr 445	Met	Pro	Gly	Leu	Gly 450
Trp	Val	Leu	Arg	Arg 455	Ser	Leu	Tyr	Lys	Glu 460	Glu	Leu	Glu	Pro	Lys 465
Trp	Pro	Thr	Pro	Glu 470	Lys	Leu	Trp	Asp	Trp 475	Asp	Met	Trp	Met	Arg 480
Met	Pro	Glu	Gln	Arg 485	Arg	Gly	Arg	Glu	Cys 490	Ile	Ile	Pro	Asp	Val 495
Ser	Arg	Ser	Tyr	His 500	Phe	Gly	Ile	Val	Gly 505	Leu	Asn	Met	Asn	Gly 510
Tyr	Phe	His	Glu	Ala 515	Tyr	Phe	Lys	Lys	His 520	Lys	Phe	Asn	Thr	Val 525
Pro	Gly	Val	Gln	Leu 530	Arg	Asn	Val	Asp	Ser 535	Leu	Lys	Lys	Glu	Ala 540
Tyr	Glu	Val	Glu	Val 545	His	Arg	Leu	Leu	Ser 550	Glu	Ala	Glu	Val	Leu 555
Asp	His	Ser	Lys	Asn 560	Pro	Cys	Glu	Asp	Ser 565	Phe	Leu	Pro	Asp	Thr 570
Glu	Gly	His	Thr	Tyr 575	Val	Ala	Phe	Ile	Arg 580	Met	Glu	Lys	Asp	Asp 585
Asp	Phe	Thr	Thr	Trp 590	Thr	Gln	Leu	Ala	Lys 595	Cys	Leu	His	Ile	Trp 600
Asp	Leu	Asp	Val	Arg 605	Gly	Asn	His	Arg	Gly 610	Leu	Trp	Arg	Leu	Phe 615
Arg	Lys	Lys	Asn	His 620	Phe	Leu	Val	Val	Gly 625	Val	Pro	Ala	Ser	Pro 630
Tyr	Ser	Val	Lys	Lys 635	Pro	Pro	Ser	Val	Thr 640	Pro	Ile	Phe	Leu	Glu 645
Pro	Pro	Pro	Lys	Glu 650	Glu	Gly	Ala	Pro	Gly 655	Ala	Pro	Glu	Gln	Thr 660

<211> 25

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
 ctagtccttc aaaactatat ggttgccctag attctctctg gaaactgact 3000
 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
 1 5 10 15
 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

<212> DNA

<213> Homo sapiens

<400> 99

gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgtagcggg 50
gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100
ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctggtggcc tgcacatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tggagctgga aggcagggtc cgcaggcgcg ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgtc gcaagaccag ttaaagaccc tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
acctggagag gaagttctcc tacgacctga gccagtgcac caatcagatg 600
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650
ggggaatgaa gctgtagctt ccagagacct gagtgaaaac aacgaccaga 700
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750
ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800
cagcaagtcc cagacaccag cccccagttc cgaagtgggt ttggattcaa 850
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcagggtgt 950
ggaagacaga cctgtaggtg gaagaggctt cgggggagcc ggagaactgg 1000
gccagacccc acaggtgcag gctgccctgt cagtgcagca ggaaaatcca 1050
gagatggagg gcctgagcg agaccagctt gtcacccccg acggacagga 1100
ggaggagcag gaagctgccg gggaaggag aaaccagcag aaactgagag 1150
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro
1				5					10					15

Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu Val Val Leu	Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln	Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro	Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly	Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala	Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu	Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu	Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp	Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys	Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn	Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg	Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
 ggatgcagaa agcctcagtg ttgctcttcc tggcctgggt ctgcttctc 50
 ttctacgctg gcattgccct cttcaccagt ggcttctctgc tcacccgttt 100
 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 ttttcgcggg ttgtgttggg gctgatagat gctctgcgat ttgacttcgc 250
 ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
 gcgcctcaag gccctcacca ctgggtcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550
agaccttttc cctggtgctt totccaaagc tttcttcttc ccatccttca 600
atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650
cccaccatgg acagtgggta atgggacgtg ctgattgctc acttcctggg 700
tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750
agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800
gagaatgaca cactgctggt agtggtctggg gaccatggga tgaccacaaa 850
tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900
tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950
gtgattcctc aagttagcct tgtgcccacg ctggccctgc tgctgggcct 1000
gcccatccca tttgggaata tcggggaagt gatggctgag ctattctcag 1050
ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100
ctccatctca atgctcagca ggtgtcccga tttcttcata cctactcagc 1150
tgctactcag gaccttcaag ctaaggagct tcactcagcty cagaacctct 1200
tctccaaggc ctctgctgac taccagtggc ttctccagag cccaagggg 1250
gctgaggcga cactgccgac tgtgattgct gagctgcagc agttcctgcg 1300
gggagctcgg gccatgtgca tcgagtcttg ggctcgtttc tctctggtcc 1350
gcatggcggg ggggtactgct ctcttggtctg ctctcctgctt tatctgcctg 1400
ctggcatctc agtgggcaat atccccaggc tttccattct gccctctact 1450
cctgacacct gtggcctggg gcctggttgg ggccatagcg tatgctggac 1500
tcctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550
gctgcagtga gctcattcct cccttttctg tggaaagcct gggctggctg 1600
ggggtccaag agggccctgg caaccctgtt tcccatccct gggcccgctc 1650
tggtactcct gctgtttcgc ttggctgtgt tcttctctga tagttttgtt 1700
gtagctgagg ccagggccac ccccttcctt ttgggctcat tcactcctgct 1750
cctggttgct cagcttcact gggagggcca gctgcttcca cctaagctac 1800
tcacaatgcc ccgccttggc acttcagcca caacaaacc cccacggcac 1850
aatggtgcat atgccctgag gcttgggaatt gggttgcttt tatgtacaag 1900
gctagctggg ctttttcatc gttgccctga agagacacct gtttgccact 1950

cctctccctg gctgagtcct ctggcatcca tgggtgggtgg tcgagccaag 2000
 aatttatggt atggagcttg tgtggcggcg ctggtggccc tgtagctgc 2050
 cgtgcgcttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100
 ccatgctctt tgtgcgctgg ggactgcccc taatggcatt gggactgct 2150
 gcctactggg cattggcgtc gggggcagat gaggctcccc cccgtctccg 2200
 ggtcctggtc tctggggcat ccatggtgct gcctcgggct gtagcagggc 2250
 tggctgcttc agggctcgcg ctgctgctct ggaagcctgt gacagtgtg 2300
 gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tctctcctt 2350
 ctgaggcccc ccacttctc aagctgactt ggattatgtg gtccctcaaa 2400
 tctaccgaca catgcaggag gagttccggg gccggttaga gaggaccaa 2450
 tctcagggtc ccctgactgt ggctgcttat cagttgggga gtgtctactc 2500
 agctgctatg gtcacagccc tcaccctgtt ggccctccca cttctgctgt 2550
 tgcagcgga gcgcacagc cttgtgttcc tgcttctgtt tctgcagagc 2600
 ttccttctcc tacatctgct tgctgctggg ataccogtca ccaccctgg 2650
 tccttttact gtgccatggc aggcagtctc ggcttgggccc ctcatggcca 2700
 cacagacctt ctactccaca ggccaccagc ctgtcttccc agccatccat 2750
 tggcatgcag ccttcgtggg attcccagag ggtcatggct cctgtacttg 2800
 gctgcctgct ttgctagtgg gagccaacac ctttgcctcc cacctcctct 2850
 ttgcagtagg ttgcccactg ctctgctct ggcccttccct gtgtgagagt 2900
 caagggctgc ggaagagaca gcagccccc gggaatgaag ctgatgccag 2950
 agtcagaccc gaggaggaag aggagccact gatggagatg cggctccggg 3000
 atgcgcctca gcacttctat gcagcactgc tgcagctggg cctcaagtac 3050
 ctctttatcc ttggtattca gattctggcc tgtgccttgg cagcctccat 3100
 ccttcgcagg catctcatgg tctggaaagt gtttgcctcc aagttcatat 3150
 ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200
 gctttggtga tgagagtga tgggtgctgt agctcctggg tcaggcagct 3250
 atttctggcc cagcagaggt agcctagtct gtgattactg gcacttggct 3300
 acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350
 atctgcaaga caggctcagc catactctta ctatcatgca gccaggggccc 3400

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu 500	Leu Gly Thr Ile	Glu 505	Leu Lys Leu Asp	Leu 510
Val Leu Leu Gly	Ala 515	Val Ala Ala Val	Ser 520	Ser Phe Leu Pro	Phe 525
Leu Trp Lys Ala	Trp 530	Ala Gly Trp Gly	Ser 535	Lys Arg Pro Leu	Ala 540
Thr Leu Phe Pro	Ile 545	Pro Gly Pro Val	Leu 550	Leu Leu Leu Leu	Phe 555
Arg Leu Ala Val	Phe 560	Phe Ser Asp Ser	Phe 565	Val Val Ala Glu	Ala 570
Arg Ala Thr Pro	Phe 575	Leu Leu Gly Ser	Phe 580	Ile Leu Leu Leu	Val 585
Val Gln Leu His	Trp 590	Glu Gly Gln Leu	Leu 595	Pro Pro Lys Leu	Leu 600
Thr Met Pro Arg	Leu 605	Gly Thr Ser Ala	Thr 610	Thr Asn Pro Pro	Arg 615
His Asn Gly Ala	Tyr 620	Ala Leu Arg Leu	Gly 625	Ile Gly Leu Leu	Leu 630
Cys Thr Arg Leu	Ala 635	Gly Leu Phe His	Arg 640	Cys Pro Glu Glu	Thr 645
Pro Val Cys His	Ser 650	Ser Pro Trp Leu	Ser 655	Pro Leu Ala Ser	Met 660
Val Gly Gly Arg	Ala 665	Lys Asn Leu Trp	Tyr 670	Gly Ala Cys Val	Ala 675
Ala Leu Val Ala	Leu 680	Leu Ala Ala Val	Arg 685	Leu Trp Leu Arg	Arg 690
Tyr Gly Asn Leu	Lys 695	Ser Pro Glu Pro	Pro 700	Met Leu Phe Val	Arg 705
Trp Gly Leu Pro	Leu 710	Met Ala Leu Gly	Thr 715	Ala Ala Tyr Trp	Ala 720
Leu Ala Ser Gly	Ala 725	Asp Glu Ala Pro	Pro 730	Arg Leu Arg Val	Leu 735
Val Ser Gly Ala	Ser 740	Met Val Leu Pro	Arg 745	Ala Val Ala Gly	Leu 750
Ala Ala Ser Gly	Leu 755	Ala Leu Leu Leu	Trp 760	Lys Pro Val Thr	Val 765
Leu Val Lys Ala	Gly 770	Ala Gly Ala Pro	Arg 775	Thr Arg Thr Val	Leu 780
Thr Pro Phe Ser	Gly	Pro Pro Thr Ser	Gln	Ala Asp Leu Asp	Tyr

				785					790					795
Val	Val	Pro	Gln	Ile 800	Tyr	Arg	His	Met	Gln 805	Glu	Glu	Phe	Arg	Gly 810
Arg	Leu	Glu	Arg	Thr 815	Lys	Ser	Gln	Gly	Pro 820	Leu	Thr	Val	Ala	Ala 825
Tyr	Gln	Leu	Gly	Ser 830	Val	Tyr	Ser	Ala	Ala 835	Met	Val	Thr	Ala	Leu 840
Thr	Leu	Leu	Ala	Phe 845	Pro	Leu	Leu	Leu	Leu 850	His	Ala	Glu	Arg	Ile 855
Ser	Leu	Val	Phe	Leu 860	Leu	Leu	Phe	Leu	Gln 865	Ser	Phe	Leu	Leu	Leu 870
His	Leu	Leu	Ala	Ala 875	Gly	Ile	Pro	Val	Thr 880	Thr	Pro	Gly	Pro	Phe 885
Thr	Val	Pro	Trp	Gln 890	Ala	Val	Ser	Ala	Trp 895	Ala	Leu	Met	Ala	Thr 900
Gln	Thr	Phe	Tyr	Ser 905	Thr	Gly	His	Gln	Pro 910	Val	Phe	Pro	Ala	Ile 915
His	Trp	His	Ala	Ala 920	Phe	Val	Gly	Phe	Pro 925	Glu	Gly	His	Gly	Ser 930
Cys	Thr	Trp	Leu	Pro 935	Ala	Leu	Leu	Val	Gly 940	Ala	Asn	Thr	Phe	Ala 945
Ser	His	Leu	Leu	Phe 950	Ala	Val	Gly	Cys	Pro 955	Leu	Leu	Leu	Leu	Trp 960
Pro	Phe	Leu	Cys	Glu 965	Ser	Gln	Gly	Leu	Arg 970	Lys	Arg	Gln	Gln	Pro 975
Pro	Gly	Asn	Glu	Ala 980	Asp	Ala	Arg	Val	Arg 985	Pro	Glu	Glu	Glu	Glu 990
Glu	Pro	Leu	Met	Glu 995	Met	Arg	Leu	Arg	Asp 1000	Ala	Pro	Gln	His	Phe 1005
Tyr	Ala	Ala	Leu	Leu 1010	Gln	Leu	Gly	Leu	Lys 1015	Tyr	Leu	Phe	Ile	Leu 1020
Gly	Ile	Gln	Ile	Leu 1025	Ala	Cys	Ala	Leu	Ala 1030	Ala	Ser	Ile	Leu	Arg 1035
Arg	His	Leu	Met	Val 1040	Trp	Lys	Val	Phe	Ala 1045	Pro	Lys	Phe	Ile	Phe 1050
Glu	Ala	Val	Gly	Phe 1055	Ile	Val	Ser	Ser	Val 1060	Gly	Leu	Leu	Leu	Gly 1065
Ile	Ala	Leu	Val	Met 1070	Arg	Val	Asp	Gly	Ala 1075	Val	Ser	Ser	Trp	Phe 1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgccct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaaac agaacgtggt ccagtggtgac gaccaaccac acgctggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aatTTTTTgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
				425					430					435	
Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gcccgtgaag cccccgcag 150
gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300
acagagacct ccgactggc ctggtggtgc tgggcgcca cgctctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400
ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggtgg 550
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650
cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700
gggcttctgc tcggccgact ccggagggc cctggtgtgc aggaaccggg 750
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800
cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850
ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tgttcagggg tgggggtggg cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15

Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

```
<210> 112
<211> 24
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

```
<400> 112
gacgtctgca acagctcctg gaag 24
```

```
<210> 113
<211> 23
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.
```

```
<400> 113
cgagaaggaa acgaggccgt gag 23
```

```
<210> 114
<211> 44
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

```
<400> 114
  tgacacttac catgctctgc acccgcagtg gggacagcca caga 44
```

```
<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens
```

```
<400> 115
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200
```

ggtcatcgtg acgggcgcca acacaggcat cggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaatcaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcgatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcatc catggctcca ccttctccag caccacactc gggcccatct 850
 tctggctgct ggtcaagagc cccgagctgg ccgcccagcc cagcacatac 900
 ctggccgtgg cggaggaact ggcggatgtt tccgaaagt acttcgatgg 950
 actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000
 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050
 gtgagggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcaactgccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300
 agaggggcca tctgatgctt ccctgggaa tctaaactgg gaatggccga 1350
 ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggg 1400
 gcctgtcggg gaggggtcca aggtgctccg tgaagagcat gggcaagttg 1450
 totgacactt ggtggattct tgggtccctg tgggaccttg tgcatgcatg 1500
 gtccctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatgggtgtg gtacagcgag ctgttgtctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctggggattgc ctggggactcc 1750
 cacccttcta tcaatttcta tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgaggagtttc ttctctacag ccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag caaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900
 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gaccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50

tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcc tggctcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttcccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aagggtgcca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000
cttcctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaacccagc tctcctgtct cccagtgaag acttggtgag cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	
				230					235					240	
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	
				245					250					255	
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	
				260					265					270	
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	
				275					280					285	
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	
				290					295					300	
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	
				305					310					315	
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	
				320					325					330	
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	
				335					340					345	
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	
				350					355					360	
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	
				365					370					375	
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	
				380					385					390	
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	
				395					400					405	
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	
				410					415					420	
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	
				425					430					435	
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	
				440					445					450	
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	
				455					460					465	
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	
				470					475					480	
Pro	Val	Ser	Gln												

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50
 gtggtggcgc tgctcatcgt ttgcgacggt ccctcagcct ctgccccaaag 100
 aaagaaggag atggtgttat ctgaaaagg tagtcagctg atggaatgga 150
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
 agatcctggc aaactcctgg cgatactoca gtgcattcac caacaggata 350
 ttttttgcca tgggtgattt tgatgaaggc tctgatgtat ttcagatgct 400
 aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
 tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
 ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
 atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
 tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
 agcgaaagat aatgtgtgtg gctggtattg gacttgttgt attattcttc 950
 agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
 ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
 ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
 gtatatattt tattacctct ttttttcaag tgatttaa atgttaatcat 1150
 ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaaat 1200
 ctgaggtatt tgaaaataat tatcctctta accttctctt ccagtgaaac 1250
 tttatggaac atttaattta gtacaattaa gtatatattata aaaattgtaa 1300
 aactactact ttgttttagt tagaacaag ctcaaaaacta ctttagtta 1350
 cttggtcatc tgattttata ttgccttata caaagatggg gaaagtaagt 1400
 cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcatc 1500
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
 ctctctctcc ttgcatatth cctactgcgc tccagcctga gtgatagagt 1650
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatthct 1700
 gcttgagtat ggtgttaact acctgtatt tagaaagatt tcagattcat 1750
 tccatctcct tagthtttctt ttaaggtgac ccatctgtga taaaaatata 1800
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtthctac 1850
 aaattagagt ttgtcactta ttccatthgt acctaaagaga aaaataggct 1900
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
 tcagcactth gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
 gaccatcttg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
 tgaggcacga gaatcacttg aactcaggag atggaggtht cagtgagccg 2150
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
1				5					10					15
Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25					30
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95					100					105

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
 aggttaacat ttcattcagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcattgaga ggcattgcta ccgaacacag aaatttgga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
 taatcttata cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttaccatct tctggagaaa attttgatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
 tcaccttctg cagaaatgca cctgtagat tattactctt cttatacaaa 900
 aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcattcacc ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400
 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
ataggacaga attattcaaa cggtatagca aatcttaggt ggcaccaaga 1650
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
ttctagagat acatataaat atattacaag atcataatta tgtattttaa 1800
atgaaacagt ttttaataatt accaagtttt ggccgggcac agtggctcac 1850
acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000
ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
atgttctttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
1 5 10 15
Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
20 25 30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	
380	385	390
Asn Glu His Lys Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg	Ala Val	
530	535	

<210> 133

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 133

gagagaagtc agcctggcag agagactctg aaatgagggg ttagaggtgt 50

tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200

tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

gttggtttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcaccagc tgtgacatct atagaccct tctgggcctg cccgctgaca 350

tccaggtgc ccaggccatg atggtgacat ccagtgcaat ctccctcctg 400

gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggata 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttget 1050
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgcctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tccactgac tgacctctg tgatcaaaga 1200
 ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcatgtctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccttgaacc tccatccac tcttggtatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

[illegible]

```
<210> 135
<211> 610
<212> DNA
<213> Homo sapiens
```

```
<400> 135
gcactgctgc tgtcccatca gctgctctga agtcccatgg tgccagaat 50
cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaagg 100
aagtcatcgc tcccgcgtggc tcagaaccat ggctgtgcca gccggcacc 150
agggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tccttgagcg agaccgcga atgtggtccc cctgcacct 250
tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350
```

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtogtgcctt tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

gggggcggggt gcctggagca cggcgctggg gccgcccga gcgctcactc 50
 gctcgcactc agtcgcggga ggcttccccg cgcggccgc gtcccgccc 100
 ctccccggca ccagaagtgc ctctgcgcgt ccgacggcga catgggctgc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggg ggcagccttc aaggctcgcca 250
 cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggg gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatgggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacctatcc tcctcccagg 700
 atagtgaata catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgctc ctgggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag octcaccacc tgcccagggg 900
 ataccgagg ccaaagtcag gcacccctg tcctatgtgg cccagcggca 950
 gccttctgag tctggggcgc atctgcttcc ggagcccagc acccccctgt 1000
 ctctccagg ccccgagac gtcttcttcc catccctgga cctgtccct 1050
 gactctcaa actttgagg catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200
 gatactgtga catcccagaa gcccgcccc tcaacccctc tggatgctac 1250
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
 ccccgtaggc gccttggtc ccccgttttg cccgaggctg ctcttctgtc 1550
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 gggaaggatga gtggagaggg gcacctgccc ccgccttcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
 1 5 10 15
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
 accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
 ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
 agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
 gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
 ccccgaaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
 cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
 toggccccct gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
 tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
 agtggctggg aagtgtgca agatttggc agaggacaaa gcagaccctg 1250
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
 ctggtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
 ccacacagcc agaattcttc acttgactca gatcaagaaa gtcaggaagc 1500
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
 gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
 <211> 451
 <212> PRT
 <213> Homo sapiens
 <400> 142

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgcca tggggccag caccctctc ctcatottgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcaactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaaggggaag aaggaatgag aagtacgata 500
 tgggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
 ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
 gcttcccag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
 aaccgaacag tgggtggacag ctgagtattc ccagcagagg ggctgatccc 900
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcaattgtgt 1000
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
 accatgtccc agagagaatg ctgaggctgc ctttgtcatt tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcca gtcgggccc catccagtgc 1150
 tcctttgatg ccagcggcac cctgacctct gaacgggcag cactccctta 1200
 ttttcccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
 ttcttcattc ttcaaagtgt ggccagttgt ggctcaaata ctctatattt 1450
 ttagccaatg gcaatcaaata tctttcagct cctttgtttc atacggaact 1500
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
 cccagacca gggctctaac cttgtatgag ggcaggccca gggagcaggc 1650
 agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15
Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttctctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg	gcctctatgg	gtgcaggatt	agttcccagt	cttactacca	550
gaaggccatc	tgggagctac	aggtgtcagc	actgggctca	gttcctctca	600
tttccatcac	gggatatggt	gatagagaca	tccagctact	ctgtcagtcc	650
tcgggctggt	tccccgggcc	cacagcgaag	tggaaaggtc	cacaaggaca	700
ggatttgtcc	acagactcca	ggacaaacag	agacatgcat	ggcctgtttg	750
atgtggagat	ctctctgacc	gtccaagaga	acgccgggag	catatcctgt	800
tccatgcggc	atgctcatct	gagccgagag	gtggaatcca	gggtacagat	850
aggagatacc	tttttcgagc	ctatatcggt	gcacctggct	accaaagtac	900
tgggaatact	ctgctgtggc	ctattttttg	gcattgttgg	actgaagatt	950
ttcttctcca	aattccagtg	gaaaatccag	gcggaactgg	actggagaag	1000
aaagcacgga	caggcagaat	tgagagacgc	ccggaaacac	gcagtggagg	1050
tgactctgga	tccagagacg	gctcacccga	agctctgcgt	ttctgatctg	1100
aaaactgtaa	cccatagaaa	agctccccag	gagggtgcctc	actctgagaa	1150
gagatttaca	aggaagagtg	tggtggcttc	tcagagtttc	caagcagggg	1200
aacattactg	ggaggtggac	ggaggacaca	ataaaagggtg	gcgcgtggga	1250
gtgtgccggg	atgatgtgga	caggaggaag	gagtacgtga	ctttgtctcc	1300
cgatcatggg	tactgggtcc	tcagactgaa	tggagaacat	ttgtatttca	1350
cattaaatcc	ccgttttatc	agcgtcttcc	ccaggacccc	acctacaaaa	1400
ataggggtct	tcctggacta	tgagtgtggg	accatctcct	tcttcaacat	1450
aaatgaccag	tcccttattt	ataccctgac	atgtcggttt	gaaggcttat	1500
tgaggcccta	cattgagtat	ccgtcctata	atgagcaaaa	tggaactccc	1550
atagtcatct	gcccagtcac	ccaggaatca	gagaaagagg	cctcttggca	1600
aagggcctct	gcaatcccag	agacaagcaa	cagtgagtcc	tcctcacagg	1650
caaccacgcc	cttcctcccc	aggggtgaaa	tgtaggatga	atcacatccc	1700
acattcttct	ttagggatat	taaggtctct	ctcccagatc	caaagtcccg	1750
cagcagccgg	ccaaggtggc	ttccagatga	agggggactg	gcctgtccac	1800
atgggagtca	ggtgtcatgg	ctgccctgag	ctgggagggg	agaaggctga	1850
cattacattt	agtttgctct	cactccatct	ggctaagtga	tcttgaaata	1900
ccacctctca	ggtgaagaac	cgtcaggaat	tcccatctca	caggctgtgg	1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
1 5 10 15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

	230		235		240
Gly Ile Leu Cys	Cys 245	Gly Leu Phe Phe	Gly Ile Val Gly Leu	Lys 255	
Ile Phe Phe Ser	Lys 260	Phe Gln Trp Lys	Ile Gln Ala Glu Leu	Asp 270	
Trp Arg Arg Lys	His 275	Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys 285	
His Ala Val Glu	Val 290	Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys 300	
Leu Cys Val Ser	Asp 305	Leu Lys Thr Val	Thr His Arg Lys Ala	Pro 315	
Gln Glu Val Pro	His 320	Ser Glu Lys Arg	Phe Thr Arg Lys Ser	Val 330	
Val Ala Ser Gln	Ser 335	Phe Gln Ala Gly	Lys His Tyr Trp Glu	Val 345	
Asp Gly Gly His	Asn 350	Lys Arg Trp Arg	Val Gly Val Cys Arg	Asp 360	
Asp Val Asp Arg	Arg 365	Lys Glu Tyr Val	Thr Leu Ser Pro Asp	His 375	
Gly Tyr Trp Val	Leu 380	Arg Leu Asn Gly	Glu His Leu Tyr Phe	Thr 390	
Leu Asn Pro Arg	Phe 395	Ile Ser Val Phe	Pro Arg Thr Pro Pro	Thr 405	
Lys Ile Gly Val	Phe 410	Leu Asp Tyr Glu	Cys Gly Thr Ile Ser	Phe 420	
Phe Asn Ile Asn	Asp 425	Gln Ser Leu Ile	Tyr Thr Leu Thr Cys	Arg 435	
Phe Glu Gly Leu	Leu 440	Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr	Asn 450	
Glu Gln Asn Gly	Thr 455	Pro Ile Val Ile	Cys Pro Val Thr Gln	Glu 465	
Ser Glu Lys Glu	Ala 470	Ser Trp Gln Arg	Ala Ser Ala Ile Pro	Glu 480	
Thr Ser Asn Ser	Glu 485	Ser Ser Ser Gln	Ala Thr Thr Pro Phe	Leu 495	
Pro Arg Gly Glu	Met 500				

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggottcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgcgc agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccc ccgccgccgt cgcctcagcc 200
gcctcggcgc ggaatgtcac cgggtggcgc ggggccgcgc ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggacgagc tccacggcc caggccccga ggaccgggccc ccgcgcgc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
 cgctcgggcc ctcgccgacc acccctcogg cggcggaacg cacttcgacc 500
 acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
 tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
 ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
 ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
 tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
 agaccacagg gcagtgtgag tgcgggccag gttatcaggg gcttcactgt 800
 gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
 gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
 aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
 aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000
 gggcataga ttacaaaaat attttatata cttttattct cttactttat 1050
 atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
 tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
 atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200
 ttcaggcatg aaacctgcta ggagggttag aaatgttctt atgtttatta 1250
 atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300
 taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
 ggtaccctaa tttatttaac tagtggttaag tagactgggt ttactctatt 1400
 taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
 aactattatg ttatttgag gtaatttaat ctagtggaaat aatgtactgt 1500
 tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550
 tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600
 acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
 tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
 agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
 taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
 ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

```

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg ccctgctctt gggggaggga gagggcgga ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacc 200
tggcccagta gttcatggct actggttccg ggaaggggccc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tccaggcac 500
cctggagtcc ggctgcccc agaactctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

```


	110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgcc tgccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcacctcat 250
 gagggaggat cgggtcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
 gctccacccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
				35					40					45					
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
				50					55					60					
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
				65					70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
				80					85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
				95					100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
				110					115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
				125					130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
				140					145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
				155					160					165					
Cys	Val	Pro	Glu	His															
				170															

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	
				20					25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	
				35					40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	
				50					55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	
				65					70					75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	
				80					85					90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	
				95					100					105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgaccaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctattttact gtacttttatg tataaaacia 750
 agtcactttt ctccaagttg tattttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgatttttgggt ataataaatg tgaggctggt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 181
 gtgttctgct ggagccgatg cc 22

 <210> 182
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 182
 gacatggaca atgacagg 18

 <210> 183
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 183
 cctttcagga tgtaggag 18

 <210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 184
 gatgtctgcc accccaag 18

<210> 185
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 185
 gcatcctgat atgacttgct acgtggc 27

<210> 186
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 186
 tacaagaggg aagaggagtt gcac 24

<210> 187
 <211> 52
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

<400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
 cc 52

<210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
 ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcc 100

cccaaagtct tctgtgtca ataactca ctgcacctgc aacctggat 150
 atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctoca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050
 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val	Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp			
	215	220			225
Gly Ile Pro Gly	Val Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp			
	230	235			240
Ile Arg Met Ile	Met Arg Asn Asn				
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt toccaaggagg gaaggcgttc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctcagagggtg acaggagggg 400
 tcagtgaacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggaggg 850
 cttocagcct gtgttccctt cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gaccccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
 cctcttttogg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

accaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
 attccacacc ttttctcctc ctcaagtgatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagaggggt tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtgcagcag cactggtaag ccaagactga gaaatacaag gttgcttgct 1450
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

cgcgctcccc gcgcgcctcc tcgggctcca cgcgctcttg cccgcagagg 50
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggctcggc cgcccgtcg cgcccgctg gcgctggcct tggcgtggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatccoga ggaaggcgtt ccgcggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtcgcac cttggtcacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggtgtg 850
cagaagaagg agtacgtgtg cccagcccc cactcggagc ccccatcctg 900
caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100
agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca 1150
ctcacatcgc tggtcctgta tgggaacaag atcaccgaga ttgccaaggg 1200
actgtttgat gggctgggtg ccctacagct gtcctcctc aatgccaaca 1250
agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300
ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctctt 1350
cgccccctg cagtcctacc agacactcca cttagcccaa aaccatttg 1400
tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450

atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500
gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550
attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600
gagaagtgtc gctgtgaggg cagcattgtg gactgctcca accagaagct 1650
ggtccgcata ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700
atgacaatga ggtatctgtt ctggaggcca ctggcatctt caagaagttg 1750
cccaacctgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800
agagggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850
ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900
ctcaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950
cacctttgcc ggctgagtt cggtgagact gctgtccctc tatgacaatc 2000
ggatcaccac catcaccctt ggggccttca ccacgcttgt ctccctgtcc 2050
accataaacc tcctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100
gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150
gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200
caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
gcgctgcccc gagcagtga cctgtatgga gacagtgggt cgatgcagca 2300
acaaggggct ccgcgccctc cccagaggca tgcccaagga tgtgaccgag 2350
ctgtacctgg aaggaaacca cctaacagcc gtgccagag agctgtccgc 2400
cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450
tgaccaatta caccttcagt aacatgtctc acctctccac tctgacctg 2500
agctacaacc ggctgaggtg catccccgtc cacgccttca acgggctgcg 2550
gtccctgcga gtgctaacc tccatggcaa tgacatttcc agcgttcctg 2600
aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650
aaccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700
ggcggggtac aaggagcctg gcatcgcccg ctgcagtagc cctgagccca 2750
tggctgacag gctcctgctc accaccccaa cccaccgctt ccagtgcaaa 2800
gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850
cccgtagaag aataacggga catgcacca ggaccctgtg gagctgtacc 2900

gctgtgcctg cccctacagc tacaagggca aggactgcac tgtgcccac 2950
aacacctgca tccagaaccc ctgtcagcat ggaggcacct gccacctgag 3000
tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050
ggcagcgggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100
aacaatgccca cctgcgtgga cgggatcaac aactacgtgt gtatctgtcc 3150
gcctaactac acaggtgagc tatgcgacga ggtgattgac cactgtgtgc 3200
ctgagctgaa cctctgtcag catgaggcca agtgcacccc cctggacaaa 3250
ggattcagct gcgagtgtgt ccctggctac agcgggaagc tctgtgagac 3300
agacaatgat gactgtgtgg cccacaagtg ccgccacggg gccagtgcg 3350
tggacacaat caatggctac acatgcacct gccccagggt cttcagtgga 3400
cccttctgtg aacaccccc acccatgggt ctactgcaga ccagcccatg 3450
cgaccagtac gagtgccaga acggggccca gtgcatctg gtgcagcagg 3500
agcccacctg ccgctgccca ccaggcttcg ccggccccag atgcgagaag 3550
ctcatcactg tcaacttcgt gggcaaagac tcctacgtgg aactggcctc 3600
cgccaagggtc cgaccccagg ccaacatctc cctgcagggt gccactgaca 3650
aggacaacgg catccttctc taaaaggag acaatgaccc cctggcactg 3700
gagctgtacc agggccacgt gcggctggtc tatgacagcc tgagttcccc 3750
tccaaccaca gtgtacagtg tggagacagt gaatgatggg cagtttcaca 3800
gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850
ggaactccaa agagcctggg gaagctccag aagcagccag cagtgggcat 3900
caacagcccc ctctaccttg gaggcacccc cacctccacc ggcctctccg 3950
ccttgcgcca gggcacggac cggcctctag gcggcttcca cggatgcac 4000
catgagggtc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050
acagtcacctg ggggtgtcac caggctgcaa gtccctgcacc gtgtgcaagc 4100
acggcctgtg ccgctccgtg gagaaggaca gcgtggtgtg cgagtgcgc 4150
ccaggctgga ccggcccact ctgcgaccag gaggcccggg acccctgcct 4200
cggccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250
tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300
gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcca 4350

catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400
 gogagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450
 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500
 gcccatcatg gaatgtcgtg ggggctgtgg gccccagtgc tgccagccca 4550
 cccgcagcaa ggggcggaaa tacgtcttcc agtgcacgga cggtcctcg 4600
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttgc 4650
 ctaagcccct gccgcctgc ctgccacctc tcggactcca gcttgatgga 4700
 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760					765	
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775					780	
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790					795	
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805					810	
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820					825	
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835					840	
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850					855	
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865					870	
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880					885	
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895					900	
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910					915	
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925					930	
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940					945	
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955					960	
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970					975	
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985					990	
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000					1005	
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015					1020	
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030					1035	
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr	Val	Cys	Lys	His 1340	Gly	Leu	Cys	Arg	Ser 1345	Val	Glu	Lys	Asp	Ser 1350
Val	Val	Cys	Glu	Cys 1355	Arg	Pro	Gly	Trp	Thr 1360	Gly	Pro	Leu	Cys	Asp 1365
Gln	Glu	Ala	Arg	Asp 1370	Pro	Cys	Leu	Gly	His 1375	Arg	Cys	His	His	Gly 1380
Lys	Cys	Val	Ala	Thr 1385	Gly	Thr	Ser	Tyr	Met 1390	Cys	Lys	Cys	Ala	Glu 1395
Gly	Tyr	Gly	Gly	Asp 1400	Leu	Cys	Asp	Asn	Lys 1405	Asn	Asp	Ser	Ala	Asn 1410
Ala	Cys	Ser	Ala	Phe 1415	Lys	Cys	His	His	Gly 1420	Gln	Cys	His	Ile	Ser 1425
Asp	Gln	Gly	Glu	Pro 1430	Tyr	Cys	Leu	Cys	Gln 1435	Pro	Gly	Phe	Ser	Gly 1440
Glu	His	Cys	Gln	Gln 1445	Glu	Asn	Pro	Cys	Leu 1450	Gly	Gln	Val	Val	Arg 1455
Glu	Val	Ile	Arg	Arg 1460	Gln	Lys	Gly	Tyr	Ala 1465	Ser	Cys	Ala	Thr	Ala 1470
Ser	Lys	Val	Pro	Ile 1475	Met	Glu	Cys	Arg	Gly 1480	Gly	Cys	Gly	Pro	Gln 1485
Cys	Cys	Gln	Pro	Thr 1490	Arg	Ser	Lys	Arg	Arg 1495	Lys	Tyr	Val	Phe	Gln 1500
Cys	Thr	Asp	Gly	Ser 1505	Ser	Phe	Val	Glu	Glu 1510	Val	Glu	Arg	His	Leu 1515
Glu	Cys	Gly	Cys	Leu 1520	Ala	Cys	Ser							

<210> 199

<211> 24

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccggt ttcctcccaa tttccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaatt 750
gtc 753

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcattccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctgagttgtt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600
 catctgatcg tggcagggtg ttatgacgag agagtccctg agaatgtgga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
 cggtgggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
 aaaaattttc ccctgaagca ttacagaaac agctctaccg atatgttacc 1050
 aaactgctgg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100
 ttatggattg tagaccaggt ttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300
 tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
 ataagagag cagggtatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210
 <211> 323

<212> PRT
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly		1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val		20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His		35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg		50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly		65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val		80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val		95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro		110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu		125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala		140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp		155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg		170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val		185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe		200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val		215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu		230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly		245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu		260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
gactacgccg atcogagacg tggctccctg ggcggcagaa ccatgttgga 50
cttcgcgatc ttccgccgta ccttcttgct ggcgttggtg ggagccgtgc 100
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
tttgcattgag ttccctggta atttgcattg gagatatggg cctgttgtct 250
ccttctggtt tggcaggcgc ctccgttgta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaaatg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtaacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1				5					10					15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100
tcagggttg tgccctctcg ctctctgacg ctcttgccg atctggtggt 150
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt ccccccgag gaggatgaca agcaggacat tcagctggtg 250
gccgcgctct ctgtcacctt gggcctcttt gcagtggagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
tgaggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
agctgtcact gaaatggctt tattcgctac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
tcccggaccc tgccgcccctg ccactatgtc ccgccgctct atgctgcttg 50
cctgggctct cccagaccctc cttcgactcg gagcgggtca ggagacagaa 100
gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc aggggtctact ggcccgcggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
catggcctaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cggcctctca 1700
 gcagcgggca cgggtggggc ggggcccggc cgcagagcat gtgctggatc 1750
 tgttctgtgt gtctgtctgt ggggtggggg aggggagga agtcttgtga 1800
 aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
 Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
 1 5 10 15
 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20 25 30
 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45
 Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50
gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
gcgccgccgc cgccgtcgct cctgcagcgc tgctgacctt gccgctagca 250
tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggtt gcccacacgg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcgggtg cggccgtgct gctggtcctc acgctgccgg 400
ggctgcccggt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500
ctcttcctcc ccgctgggga tatcggtccg ggcgccaac tccaaggtcg 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tgttactcgt gaagctgccg cgaatgggtg cctgctctac ctagataaaag 850
aggataagggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900
cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtggccat gactgeggcc gtgttcttcg gctgcgccctt cattgccttc 50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcacgcgcg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg ctggggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt gggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tgggtgctcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgtccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15
Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255
Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
cggaaccag cgcgcgcac caccgtgcc actgcgccc tgccggggcc 50
atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100
gagccatctg ggggttcttg ggccaagaa cgtctcgag aaagacgccg 150
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtctgaaca agcagaaggg ggcgcggtt ctgtttgtgg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350
gggatgtttc agcgcaagta cctctaccaa aaagtgaac gaaccctgtg 400
tcagcccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450
tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
agcagcacag cccagtaact tcaagtatga gttccctgaa ggcgtggact 600
cgtaattgt caaggtgacc tocaacaagg ccttcccctg ctcagtcac 650
tccattcagg atgtgctgtg tctgtctat gacctggaca acaacgtagc 700
cttcacggc atgtaccaga cgatgaccaa gaaggcggcc atcacgtac 750
agcgcaaaga cttcccagc aacagctttt atgtggtggt ggtggtgaag 800
accgaagacc aagcctgcgg gggctccctg cctttctacc ccttcgcaga 850
agatgaaccg gtcgatcaag ggcaccgcca gaaaaccctg tcagtgtgtg 900
tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctcttttgc 950
ctgggtatat ttctctcctt ttacctgtg accgtcctcc tggcctgtg 1000
ggagaactgg aggcagaaga agaagaccct gctggtggcc attgaccgag 1050
cctgccaga aagcgtcac cctcgagtc tggctgattc ttttcttggc 1100
agttcccctt atgagggtta caactatggc tcctttgaga atgtttctgg 1150
atctaccgat ggtctggttg acagcgctgg cactggggac ctctcttacg 1200
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350

tggcacggaa ggacaagcgt gttctgcgga aaaagtacca gatctacttc 1400
 tggaacattg ccaccattgc tgtctttctat gcccttcctg tgggtgcagct 1450
 ggtgatcacc taccagacgg tggatgaatgt cacaggggaat caggacatct 1500
 gctactacaa cttcctctgc gccacccac tgggcaatct cagcgccttc 1550
 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttcct 1600
 gctcatcatc ctgcaacggg agatcaacca caaccgggac ctgctgcgca 1650
 atgacctctg tgccctggaa tgtgggatcc ccaaactt tgggcttttc 1700
 tacgccatgg gcacagccct gatgatggag gggctgctca gtgcttgcta 1750
 tcatgtgtgc cccaactata ccaatttcca gtttgacaca tcgttcatgt 1800
 acatgatcgc cggactctgc atgctgaagc tctaccagaa gcggcaccgc 1850
 gacatcaacg ccagcgccta cagtgcctac gcctgcctgg ccattgtcat 1900
 cttcttctct gtgctgggag tggcttttg caaaggggaa acggcgcttc 1950
 ggatcgtctt ctccatcatt cacatcatcg ccacctgct cctcagcacg 2000
 cagctctatt acatgggccc gtggaaactg gactcgggga tcttcgccg 2050
 catcctccac gtgctctaca cagactgcat ccggcagtg agcgggcccgc 2100
 tctacgtgga ccgcatgggt ctgctgggca tgggcaacgt catcaactgg 2150
 tcgctggctg cctatgggct tatcatgcgc ccaatgatt tcgcttccta 2200
 cttgttgccc attggcatct gcaacctgct cctttacttc gccttctaca 2250
 tcatcatgaa gctccggagt ggggagagga tcaagctcat cccctgctc 2300
 tgcacggttt gcacctcgt ggtctggggc ttgcgctct tcttcttctt 2350
 ccagggactc agcacctggc agaaaacccc tgcagagtcg agggagcaca 2400
 accgggactg catcctcctc gacttctttg acgaccaoga catctggcac 2450
 ttctctcct ccacgcccgt gttcgggtcc ttctggtgt tgctgacact 2500
 ggatgacgac ctggatactg tgcagcggga caagatctat gtcttctagc 2550
 aggagctggg cccttcgctt cacctcaagg ggccctgagc tcctttgtgt 2600
 catagaccgg tcaactctgc gtgctgtggg gatgagtccc agcaccgctg 2650
 cccagcactg gatggcagca ggacagccag gtctagctta ggcttggcct 2700
 gggacagcca tggggtggca tggaaacttg cagctgccct ctgccgagga 2750
 gcaggcctgc tccctggaa ccccagatg ttggccaaat tgctgctttc 2800

ttctcagtgt tggggccttc catgggcccc tgtcctttgg ctctccattt 2850
gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900
ttgcattttg cccgtcctcc tccccacaat gccccagcct gggacctaag 2950
gcctcttttt cctcccatat tcccactcca gggcctagtc tggggcctga 3000
atctctgtcc tgtatcaggg ccccagttct ctttgggctg tccctggctg 3050
ccatcactgc ccattccagt cagccaggat ggatgggggt atgagatttt 3100
gggggtttgc cagctgggtgc cagacttttg gtgctaaggc ctgcaagggg 3150
cctggggcag tgcgtattct cttccctctg acctgtgctc agggctggct 3200
cttttagcaat gcgctcagcc caatttgaga accgccttct gattcaagag 3250
gctgaattca gaggtcacct cttcatcca tcagctcca gactgatgcc 3300
agcaccagga ctggaggagg aagcgcctca ccccttcctt tccttctttc 3350
caggccctta gtcttgccaa accccagctg gtggcctttc agtgccattg 3400
acactgcca agaattgtcca ggggcaaagg agggatgata cagagttcag 3450
cccgttctgc ctccacagct gtgggcaccc cagtgcctac cttagaaagg 3500
ggcttcagga agggatgtgc tgtttccctc tacgtgcca gtcctagcct 3550
cgctctagga ccagggctg gcttctaagt ttccgtccag tcttcaggca 3600
agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagtttac 3650
aaagaattgc ccagctctg ggcaccctgg ccaccctggt ccttgatcc 3700
ccttcgtccc acctgggtcca cccagatgc tgaggatggg ggagctcagg 3750
cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttgttt 3800
ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850
tcagagcgtc tocatgctat ggttgcattt ccgttttcta tgaatgaatt 3900
tgattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1				5				10					15	
Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
			20					25					30	

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				

				320					325					330
Ile	Asp	Arg	Ala	Cys 335	Pro	Glu	Ser	Gly	His 340	Pro	Arg	Val	Leu	Ala 345
Asp	Ser	Phe	Pro	Gly 350	Ser	Ser	Pro	Tyr	Glu 355	Gly	Tyr	Asn	Tyr	Gly 360
Ser	Phe	Glu	Asn	Val 365	Ser	Gly	Ser	Thr	Asp 370	Gly	Leu	Val	Asp	Ser 375
Ala	Gly	Thr	Gly	Asp 380	Leu	Ser	Tyr	Gly	Tyr 385	Gln	Gly	Arg	Ser	Phe 390
Glu	Pro	Val	Gly	Thr 395	Arg	Pro	Arg	Val	Asp 400	Ser	Met	Ser	Ser	Val 405
Glu	Glu	Asp	Asp	Tyr 410	Asp	Thr	Leu	Thr	Asp 415	Ile	Asp	Ser	Asp	Lys 420
Asn	Val	Ile	Arg	Thr 425	Lys	Gln	Tyr	Leu	Tyr 430	Val	Ala	Asp	Leu	Ala 435
Arg	Lys	Asp	Lys	Arg 440	Val	Leu	Arg	Lys	Lys 445	Tyr	Gln	Ile	Tyr	Phe 450
Trp	Asn	Ile	Ala	Thr 455	Ile	Ala	Val	Phe	Tyr 460	Ala	Leu	Pro	Val	Val 465
Gln	Leu	Val	Ile	Thr 470	Tyr	Gln	Thr	Val	Val 475	Asn	Val	Thr	Gly	Asn 480
Gln	Asp	Ile	Cys	Tyr 485	Tyr	Asn	Phe	Leu	Cys 490	Ala	His	Pro	Leu	Gly 495
Asn	Leu	Ser	Ala	Phe 500	Asn	Asn	Ile	Leu	Ser 505	Asn	Leu	Gly	Tyr	Ile 510
Leu	Leu	Gly	Leu	Leu 515	Phe	Leu	Leu	Ile	Ile 520	Leu	Gln	Arg	Glu	Ile 525
Asn	His	Asn	Arg	Ala 530	Leu	Leu	Arg	Asn	Asp 535	Leu	Cys	Ala	Leu	Glu 540
Cys	Gly	Ile	Pro	Lys 545	His	Phe	Gly	Leu	Phe 550	Tyr	Ala	Met	Gly	Thr 555
Ala	Leu	Met	Met	Glu 560	Gly	Leu	Leu	Ser	Ala 565	Cys	Tyr	His	Val	Cys 570
Pro	Asn	Tyr	Thr	Asn 575	Phe	Gln	Phe	Asp	Thr 580	Ser	Phe	Met	Tyr	Met 585
Ile	Ala	Gly	Leu	Cys 590	Met	Leu	Lys	Leu	Tyr 595	Gln	Lys	Arg	His	Pro 600
Asp	Ile	Asn	Ala	Ser 605	Ala	Tyr	Ser	Ala	Tyr 610	Ala	Cys	Leu	Ala	Ile 615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
				815					820					825	
Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

gctcaagtgc cctgccttgc cccaccagc ccagcctggc cagagcccc 50

tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100

ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350
 ctggcttctt gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcacctt ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
 ggcatccctt tctcttctt tgaggcttca gaccgggatg agccaggcac 600
 agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650
 cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700
 agccccagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750
 gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg 800
 ccaactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850
 gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat 900
 ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950
 atccccggg accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000
 agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050
 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100
 tggatgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150
 acagtacgca tccctgagct cagtccacca ggtactgaag tgactagact 1200
 gtcagcagag gatgcagatg cccccggctc ccccaattcc cacgttgtgt 1250
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tccactccg 1350
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
 ttgatgctga cctcgagccc gccttcgcc tcatggattt tgccattgag 1600
 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

gcacgtttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700
gtcatgaggt ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca 1750
ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt 1800
gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850
tcagtgcgcc agccggctct ttcctgctga ccatccagcc ctccgacccc 1900
atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctgggt 1950
ctgcattgag aaattctccg gggaggtgca caccgcccag tccctgcagg 2000
gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggatata 2050
gccctgactc ttgcccctgt gccctcccaa tacctctgca caccgcca 2100
agaccatggc ttgatcgtga gtggaccag caaggacccc gatctggcca 2150
gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa 2200
cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250
ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtggtggtca 2300
gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350
tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaaggcat 2400
gcccacgaag ctgtcggcag tgggcatect ttaggcacc ctggtagcaa 2450
taggaatctt cctcatcctc attttcacc actggaccat gtcaaggaag 2500
aaggaccggt atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550
aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag 2600
tccctggga gagagcccag caccgaagat ccagcagggg acaggacaga 2650
gtagaagccc ctccatctgc cctgggggtg aggcaccatc accatcacca 2700
ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750
gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800
ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229
<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
1 5 10 15
Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	320	325	330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	335	340	345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	350	355	360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	365	370	375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	380	385	390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	395	400	405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	410	415	420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	425	430	435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	440	445	450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	455	460	465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	470	475	480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	485	490	495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	500	505	510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	515	520	525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	530	535	540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	545	550	555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	560	565	570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	575	580	585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	590	595	600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly			

	605		610		615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp			
	620	625		630	
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu			
	635	640		645	
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His			
	650	655		660	
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser			
	665	670		675	
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val			
	680	685		690	
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr			
	695	700		705	
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile Ile			
	710	715		720	
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val			
	725	730		735	
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg			
	740	745		750	
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val			
	755	760		765	
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile			
	770	775		780	
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp			
	785	790		795	
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800	805			

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
 cgccttaccg cgcagcccgga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Segeunce

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aacccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
 ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
 atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caattttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcattttaa at ccttctgag 250
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctattttacca 400
 cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
 actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatoca 550
 ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
 ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
 atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700
 tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750
 gtcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
 ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atcaaaaaac 900
atgggaattt caagggcttc atcgacctgc acagctactc gcagctgctg 950
atgtatccat atgggtactc agtcaaaaag gcccagatg ccgaggaact 1000
cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100
agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
tgagttgaga gataccggga cctatggctt cctcctgcc gctaaccaga 1200
tcatcccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250
catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
atttgtacct acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350
cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400
cccctctcca gccagctccc tggagtcgtg tgtcctggcg gtgtccctgc 1450
aagaactgggt tctgccagcc tgctcaattt tggctcctgct gtttttgatg 1500
agccttttgt ctgtttctcc ttccaccctg ctggctgggc ggctgcactc 1550
agcatcacc cttcctgggt ggcatgtctc tctctacctc attttttagaa 1600
ccaaagaaca tctgagatga ttctctaccc tcatccacat ctagccaagc 1650
cagtgcactt gctctgggtg cactgtggga gacaccactt gtcttttaggt 1700
gggtctcaaa gatgatgtag aatttccttt aatttctogc agtcttcctg 1750
gaaaatattt tcctttgagc agcaaactct gtagggatat cagtgaaggt 1800
ctctccctcc ctctctctct gttttttttt tttttgagac agagttttgc 1850
tcttgttgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900
ctctgcctcc tgggttcaag caattctcct gcctcagcct cttgagtagc 1950
ttggtttata ggcgatgcc accatgcctg gctaattttg tgtttttagt 2000
agagacaggg tttctccatg ttggtcaggc tgggtctaaa ctcccaacct 2050
caggtgatct gccctccttg gcctcccaga gtgctgggat tacaggtgtg 2100
agccactgtg ccgggcccggt cccctccttt tttaggcctg aatacaaagt 2150
agaagatcac tttccttcac tgtgctgaga atttctagat actacagttc 2200
ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250
gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300

atctaaattg caggatgggtg aaattatccc catctgtcct aatgggotta 2350
 cctcctcttt gccttttgaa ctcaattcaa agatctaggc ctcatcttac 2400
 aggtcctaaa tcaactcatct ggcttgata atctcactgc cctggcacat 2450
 tcccatttgt gctgtgggtg atcctgtgtt tccttgcctt ggtttgtgtg 2500
 tgtgtgtgtg tgtgtgtgtg tgtgtgtgtt tgtgtgtgtg tgtctgtcta 2550
 ttttgtatcc tggaccacaa gttcctaagt agagcaagaa ttcatcaacc 2600
 agctgcctct tgtttcattt cacctcagca cgtaccatct gtccttttgt 2650
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700
 tottaacctc ctgcctagga tttgtacagc atctgggtgtg tgcttataag 2750
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
 1 5 10 15

Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
 20 25 30

Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60

Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75

Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90

Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105

Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120

Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135

Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150

His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

aatcaccaaa ccatcaacag ggacccagc cacaagccaa caccattaa 1500
 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys	1	5	10	15
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr	20	25	30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	35	40	45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	50	55	60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	65	70	75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	80	85	90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	95	100	105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	110	115	120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	125	130	135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	140	145	150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	155	160	165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	170	175	180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	185	190	195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala				

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe
	215	220 225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met Met
	230	235 240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn
	245	250 255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe
	260	265 270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala
	275	280 285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys
	290	295 300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser
	305	310 315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala
	320	325 330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser
	335	340 345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser
	350	355 360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile
	365	370 375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn
	380	385 390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile
	395	400 405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser
	410	415

<210> 237
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 237
 caaccatgca aggacagggc agg 23

 <210> 238

agctgcccac gcctgagtc aagattcttc ccaggaacac aaacgtagga 100
gaccacagct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300
aacaattcc aatgagacta gcacctctgc caaacttga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
ctgggtccag tgtgacctcc agtggagcca gcactgccac caactctgag 700
tccagcacag tgtccagttag ggccagcact gccaccaact ctgagtctag 750
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800
cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850
agtggggcca gcacagccac caactctgag tccagcacag tgtccagttag 900
ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
gccaccaact ctgagtccag cagacctcc agtggggcca gcacagccac 1050
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100
ctgagtccag cagacctcc agtggggcca gcacagccac caactctgag 1150
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400
gcactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

				365					370					375
Thr	Asn	Ser	Glu	Ser 380	Ser	Thr	Val	Ser	Ser 385	Gly	Ala	Ser	Thr	Ala 390
Thr	Asn	Ser	Glu	Ser 395	Ser	Thr	Thr	Ser	Ser 400	Gly	Val	Ser	Thr	Ala 405
Thr	Asn	Ser	Glu	Ser 410	Ser	Thr	Thr	Ser	Ser 415	Gly	Ala	Ser	Thr	Ala 420
Thr	Asn	Ser	Asp	Ser 425	Ser	Thr	Thr	Ser	Ser 430	Glu	Ala	Ser	Thr	Ala 435
Thr	Asn	Ser	Glu	Ser 440	Ser	Thr	Val	Ser	Ser 445	Gly	Ile	Ser	Thr	Val 450
Thr	Asn	Ser	Glu	Ser 455	Ser	Thr	Thr	Ser	Ser 460	Gly	Ala	Asn	Thr	Ala 465
Thr	Asn	Ser	Gly	Ser 470	Ser	Val	Thr	Ser	Ala 475	Gly	Ser	Gly	Thr	Ala 480
Ala	Leu	Thr	Gly	Met 485	His	Thr	Thr	Ser	His 490	Ser	Ala	Ser	Thr	Ala 495
Val	Ser	Glu	Ala	Lys 500	Pro	Gly	Gly	Ser	Leu 505	Val	Pro	Trp	Glu	Ile 510
Phe	Leu	Ile	Thr	Leu 515	Val	Ser	Val	Val	Ala 520	Ala	Val	Gly	Leu	Phe 525
Ala	Gly	Leu	Phe	Phe 530	Cys	Val	Arg	Asn	Ser 535	Leu	Ser	Leu	Arg	Asn 540
Thr	Phe	Asn	Thr	Ala 545	Val	Tyr	His	Pro	His 550	Gly	Leu	Asn	His	Gly 555
Leu	Gly	Pro	Gly	Pro 560	Gly	Gly	Asn	His	Gly 565	Ala	Pro	His	Arg	Pro 570
Arg	Trp	Ser	Pro	Asn 575	Trp	Phe	Trp	Arg	Arg 580	Pro	Val	Ser	Ser	Ile 585
Ala	Met	Glu	Met	Ser 590	Gly	Arg	Asn	Ser	Gly 595	Pro				

<210>	244
<211>	26
<212>	DNA
<213>	Art

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	
1				5					10					15	
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	
				20					25					30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	
				35					40					45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	
				50					55					60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	
				65					70					75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	
				80					85					90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	
				95					100					105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	
				110					115					120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
				125					130					135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	
				140					145					150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	
				155					160					165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	
				170					175					180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 251
 tgacccatt gagaaggatca ttgaaggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggcccccgc ggggggcgat gaccgtgcgc 100
tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggaacc gcggggcgga gctgccgcc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcga 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgcgc 300
cctcgggcac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
gccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450
acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
agaggccctc tttgcaactca gtagcaacct cagcttcctg ccaggcgggg 550
agtaccagga gctgcttttg ggtgcagacg cagagaagaa acagcagtgc 600
agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat 650
cctcctgccg ctacgcggca gtcacctgtt cacctgtggc acagcagcct 700
tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800
cgacccgaat ttcaagtcca ctgccctggt ggttgatggc gagctctaca 850
ctggaacagt cagcagcttc caagggaatg acccggccat ctgcgggagc 900
caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga 950
cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050
tttgagttct ttgagaacac cattgtgtcc cgcattgcc gcctctgcaa 1100
gggcgatgag ggtggagagc gggtgctaca gcagcgctgg acctccttcc 1150
tcaaggcca gctgctgtgc tcacggcccc acgatggctt ccccttcaac 1200
gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250
cacccttttc tatgggtctc tcaactccca gtggcacagg ggaactacag 1300
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350
agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400
gaccacccg gtgccacac ccggcctgg agcgtgcac accaacagtg 1450

ctctccagtc aagtagcgaa gtcctacca cccagacacc caaacagccg 2950
 tggccccaga ggtcctggcc aaatatgggg gcctgcctag gttggtggaa 3000
 cagtgcctct tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050
 gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100
 ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150
 ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200
 acattatccc gctgccaccg gctgccctgt ctactgcag attcaggacc 3250
 agcttgggct gcgtgcgttc tgccttgcca gtcagccgag gatgtagttg 3300
 ttgctgccgt cgtcccacca cctcaggac cagagggcta ggttggcact 3350
 gcggccctca ccaggtcctg ggctcggacc caactcctgg acctttccag 3400
 cctgtatcag gctgtggcca cacgagagga cagcgcgagc tcaggagaga 3450
 tttcgtgaca atgtacgctt ttcctcaga attcaggga gagactgtcg 3500
 cctgccttcc tccgttggtg cgtgagaacc cgtgtgcccc tcccaccat 3550
 atccaccctc gctccatctt tgaactcaaa cacgaggaac taactgcacc 3600
 ctggtcctct cccagtccc cagttcacc tccatccctc accttcctcc 3650
 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700
 gtttttatac attttttaaat aagatgcact ttatgtcatt ttttaataaa 3750
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
1				5					10					15
Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val Val			

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
 cgcccgagcc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250
 caggccgcgg cggcgggggc ggggtgtgcg aacaaagcgc cggcgcgggg 300
 cctgcggggc gctcgggggc cgcgatgggc gcggcgggcc cgcggcgggc 350
 gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400
 tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcgggcggc 450
 ggcggcgggc gcggccccgc gggcgagcgg gcgcgggcgt ggccgcgcgc 500
 ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550
 gctggcctcg cggctcgtcc tgccccgggc ttccgagctg aagcgagcgg 600
 gcccacggcg ccgcgccagc cccgagggtc gccgggtccg gcaggcgggc 650
 gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700
 gccgccccgc tcggaccagc atggcgggcc gcgcgacagg aacttttctc 750
 tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800
 gcctacagaa catggtccaa gacaattcct gggaaagtcc agttcttctc 850
 aagtgagggc tctgacacat ctgtaccaat tccagtagtg ccactacggg 900
 gtgtggacga ctctaccgc cccagaaga agtccttcat gatgctcaag 950
 tacatgcacg accactactt ggacaagtat gaatggttta tgagagcaga 1000
 tgatgacgtg tacatcaaag gagaccgtct ggagaacttc ctgaggagtt 1050
 tgaacagcag cgagcccctc tttcttgggc agacaggcct gggcaccacg 1100
 gaagaaatgg gaaaactggc cctggagcct ggtgagaact tctgcatggg 1150
 ggggcctggc gtgatcatga gccgggaggt gcttcggaga atggtgccgc 1200
 acattggcaa gtgtctccgg gagatgtaca ccacccatga ggacgtggag 1250
 gtgggaaggc gtgtccggag gtttgcaggc gtgcagtggt tctggtctta 1300
 tgagatgcgg cagctttttt atgagaatta cgagcagaac aaaaaggggt 1350
 acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400
 cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450
 ccgcaagata tccgagctcc gccatgcac aatacagctg caccgcgaaa 1500
 ttgtcctgat gagcaaatac agcaacacag aaattcataa agaggacctc 1550
 cagctgggaa tccctccctc cttcatgagg ttccagcccc gccagcgaga 1600

attcctgttt tagctgaaga attgtattac atttggagag taaaaaactt 4550

aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

				530					535					540
Ser	Gly	Arg	Phe	Asp 545	Met	Phe	Val	Arg	Phe 550	Met	Gly	Asn	Phe	Glu 555
Lys	Thr	Cys	Leu	Ile 560	Pro	Asn	Gln	Asn	Val 565	Lys	Leu	Val	Val	Leu 570
Leu	Phe	Asn	Ser	Asp 575	Ser	Asn	Pro	Asp	Lys 580	Ala	Lys	Gln	Val	Glu 585
Leu	Met	Arg	Asp	Tyr 590	Arg	Ile	Lys	Tyr	Pro 595	Lys	Ala	Asp	Met	Gln 600
Ile	Leu	Pro	Val	Ser 605	Gly	Glu	Phe	Ser	Arg 610	Ala	Leu	Ala	Leu	Glu 615
Val	Gly	Ser	Ser	Gln 620	Phe	Asn	Asn	Glu	Ser 625	Leu	Leu	Phe	Phe	Cys 630
Asp	Val	Asp	Leu	Val 635	Phe	Thr	Thr	Glu	Phe 640	Leu	Gln	Arg	Cys	Arg 645
Ala	Asn	Thr	Val	Leu 650	Gly	Gln	Gln	Ile	Tyr 655	Phe	Pro	Ile	Ile	Phe 660
Ser	Gln	Tyr	Asp	Pro 665	Lys	Ile	Val	Tyr	Ser 670	Gly	Lys	Val	Pro	Ser 675
Asp	Asn	His	Phe	Ala 680	Phe	Thr	Gln	Lys	Thr 685	Gly	Phe	Trp	Arg	Asn 690
Tyr	Gly	Phe	Gly	Ile 695	Thr	Cys	Ile	Tyr	Lys 700	Gly	Asp	Leu	Val	Arg 705
Val	Gly	Gly	Phe	Asp 710	Val	Ser	Ile	Gln	Gly 715	Trp	Gly	Leu	Glu	Asp 720
Val	Asp	Leu	Phe	Asn 725	Lys	Val	Val	Gln	Ala 730	Gly	Leu	Lys	Thr	Phe 735
Arg	Ser	Gln	Glu	Val 740	Gly	Val	Val	His	Val 745	His	His	Pro	Val	Phe 750
Cys	Asp	Pro	Asn	Leu 755	Asp	Pro	Lys	Gln	Tyr 760	Lys	Met	Cys	Leu	Gly 765
Ser	Lys	Ala	Ser	Thr 770	Tyr	Gly	Ser	Thr	Gln 775	Gln	Leu	Ala	Glu	Met 780
Trp	Leu	Glu	Lys	Asn 785	Asp	Pro	Ser	Tyr	Ser 790	Lys	Ser	Ser	Asn	Asn 795
Asn	Gly	Ser	Val	Arg 800	Thr	Ala								

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggctcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gtttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500
 tggctgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatataa gtcacctgtc accactttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750
 aaactgcatg agaaaaaccc gaagagtttg gaaagcacc agagagttgg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgc 850
 acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300
 ataaaaatat tttctattgt agttcaaagt tgccaacatc tttatgtgtc 1350
 atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataa 1400
 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	50	55	60
65	70	75	
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

cggctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc tgacctcaa atcatccatc caccctgct gtcattctgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcaactg 200
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tgggtccacct ctacagagat ggggaagact 350
gggaatctaa gcagatgcc aagtatcgag ggagaactga gtttgtgaag 400
gactccattg caggggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttaogatg 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600
ctcaggctgg tttccccagc ccacagccaa gtggaaaggt ccacaaggac 650
aggatttgtc ttcagactcc agagcaaagt cagatgggta cagcctgtat 700
gatgtggaga tctccattat agtcaggaa aatgctggga gcatattgtg 750
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga 800
taggagagac gtttttccag ccctcacctt ggcgctggc ttctatttta 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000
gtgactctgg atccagagac ggctcaccg aagctctgcg tttctgatct 1050
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ocaacaatgg gtattgggtc ctgagactga caacagaaca tttgtatttc 1300
 acattcaatc cccattttat cagcctcccc cccagcaccc ctctacacg 1350
 agtaggggtc ttcctggact atgagggtgg gaccatctcc ttcttcaata 1400
 caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
 ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500
 tcccatattc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550
 cttaaagggc cccacaccac agaccagac acagccaagg gagagtgctc 1600
 cogacaggtg gcccagctt cctctccgga gcctgcgcac agagagtca 1650
 gcccccaact ctcttttagg gagctgaggt tcttctgccc tgagccctgc 1700
 agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750
 gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800
 ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
 cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900
 tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
 tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
 accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050
 aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
 ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
 gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
 gtccatatcc ctcatthaaca cagacacaaa aattctaaat aaaattttta 2250
 caaattaaac taaacaatat atttaaagat gatataatac tactcagtgt 2300
 ggtttgtccc acaaatgcag agttggttta atattttaa atcaaccagt 2350
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aaa 2403

<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
 1 5 10 15
 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser Cys	Ser Leu Phe Pro Glu
35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln Phe
50	55	60
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser
65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp
80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr
95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile
110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly
125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile
140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala
155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg
170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile
185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu
200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu
215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu
230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile
245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp
260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys
275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys
290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro
305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50
 tgggtgagggc taggaaaaga gtttgttggg aaccctgggt tatcggcctc 100
 gtcattcttca tatccctgat tgcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct cagggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
ctagcctgca gtgggatggg agtcatcgct gtggagcaac ctttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt ttacaacat ataagaaccc 750
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950
caggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
tatgtgotgg ctcttagaa ggaaaaacag atgcatgcca gggtgactct 1150
ggaggaccac tggtagttc agatgctaga gatctctggt accttgctgg 1200
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250
atactagagt tacggccttg cgggactgga ttacttcaa aactgggtatc 1300
taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg 1350
gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400
gotagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
ttcccagctc tggtccgcac gtaagcatcc tgcttctgcc agatcaactc 1500
tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600
cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750
tcccctacat ttatttgga cagaaaagta ttaggtgttt ttcttagtgg 1800
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gtttaaggaag 1900
tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatattat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
 gtogaaggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50
 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100
 cagacgtcag ctggtggatt cccgctgcat caaggcctac cactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
 ttcccagagc tcagcccttg gcccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gacccgcgcg gcattgggaga agtgcgcatg gcggccgaag agggccgcgc 450
agtgggtccac tgggtgtgccc ccttctcccc ggtcctccac tactggctgc 500
tgctttggga cggcagcgag gctgcgaga aggggcccc gctgaacgct 550
acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
ctggaggaga gggcctcgag ggggcccaga tccctgcctt cgggccttgc 700
agccgccttg cggtgccgcc caacccccgc actctggtcc acgcggccgt 750
cgggggtggc acggccctgg cctgctaag ctgtgccgcc ctggtgtggc 800
acttctgcct gcgcgatcgc tggggctgcc cgcgcgagc cgcgcgccga 850
gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900
ccccacctgg ggcgctcagc ctggccccgc ggaaagagga aaacccgctg 950
cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000
gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050
acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150
ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
1 5 10 15
Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
 agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg 50
 cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100
 cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250
 acgccctcaa tctgtctttt tggttaatgt ccatcagtgt gttggcagtt 300
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcatc 400
 cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttggtgc gtttggacat 550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttcgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gttaaaggtg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700
tgatcagggg ttttttgtat ataagtctgt gttaaactctg tataattcag 1750
tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800
ttgtcctgta tagcatcatt attttagcc tttcctgtta ataaagcttt 1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggctcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttagt tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gottatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
1				5					10					15
Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His Gln			
	185	190			195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys Met			
	200	205			210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg Phe			
	215	220			225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile Leu			
	230	235			240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu Pro			
	245	250			255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln His			
	260	265			270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser Arg			
	275	280			285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His Phe			
	290	295			300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
 gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgagggac 50
 caaggcctgc cctgcactcg ggccctctcc agccagtgtc gaccagggac 100
 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150
 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gaggatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
 cgggcagcct ctccattca tcccaggaa gcagctgtgt gacggagagc 450
 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttogacaact 600

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtggggcc tgtctctcag 750
 gctccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800
 ccccggtgtg tgggtgggga ggaggcctct gtggattctt ggccctggca 850
 ggtcagcatc cagtagcaca aacagcacgt ctgtggaggg agcatcctgg 900
 acccccactg ggtcctcacg gcagccact gcttcaggaa acataccgat 950
 gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
 atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
 ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
 tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
 tcagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200
 gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350
 acagtgggtg gccctgatg taccaatctg accagtggca tgtggtgggc 1400
 atcgttagct ggggctatg ctgcgggggc ccgagcacc caggagtata 1450
 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
 agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc ttccctcctg 1550
 ccctgcccac ctggggatcc ccaaagtca gacacagagc aagagtcccc 1600
 ttgggtacac ccctctgccc acagcctcag catttcttg agcagcaaag 1650
 ggctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
 gtcagcagcc ctagctcggc cacacttggg gctcccagca tcccaggag 1750
 agacacagcc cactgaacaa ggtctcagg gtattgctaa gccaagaagg 1800
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcacca tccccagcc tactagagca agaaaccagt tgtaataata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
1 5 10 15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

265

1005610100

Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	425	430	

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
 gggctgaggc actgagagac cggaaagcct ggcattccag agggagggaa 50
 acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100
 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctccctgggcc 150
 ttttctcttt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggcccat gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gagtgggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
tgcttgtacc ttcatggaac ttcaagattc ctacctgttg cccatctcgg 600
aggacaaggt catggaggga aaaggccaaa gcccctttga ccccgctcac 650
aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700
caacttctcg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttctccgct ggctgcatca tgacgcctcc 800
tttgtggcag ccatcccttc gaccaggtc gtctacttct tcttcgagga 850
gacagccagc gagtttgact tctttgagag gctccacaca tcgcgggtgg 900
ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950
tggaccacct tcctgaaggc ccagctgctc tgcaccagc cggggcagct 1000
gcccttcaac gtcacccgcc acgcggtcct gctccccgcc gattctccca 1050
cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100
accaggagct ctgcggtttg tgccttctct ctcttggaac ttgaacgtgt 1150
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200
cttatagggg ccctgagacc aacccccggc caggcagttg ctcagtgggc 1250
ccctcctctg ataaggccct gaccttcatt aaggaccatt tcctgatgga 1300
tgagcaagtg gtggggacgc ccctgctggt gaaatctggc gtggagtata 1350
cacggcttgc agtggagaca gccaggggcc ttgatgggca cagccatctt 1400
gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450
tggggacagc agtgcctatc tgggtgaaga gattcagctg ttccctgacc 1500
ctgaacctgt tcgcaacctg cagctggccc ccaccaggg tgcaagtgtt 1550
gtaggcttct caggaggtgt ctggagggtg ccccgagcca actgtagtgt 1600
ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgoc 1650
gggaccctga gtcccgaacc tgttgcttcc tgtctgcccc caacctgaac 1700
tcctggaagc aggacatgga gcgggggaac ccagagtggg catgtgccag 1750
tggcccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800
aagaagtcct ggctgtcccc aactccatcc tggagctccc ctgccccac 1850

ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtccc 1900
agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
atggagttgg gggctcttac cagtgcctgg caactgagaa tggcttttca 2000
taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050
ggatcctgaa ctggcaggca tcccccgga gcatgtgaag gtcccgttga 2100
ccagggtcag tgggtggggcc gccctggctg cccagcagtc ctactggccc 2150
cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200
catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250
ttcagggtcg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300
gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350
ggacgctgac aacaactgcc taggcactga ggtagcttaa actctaggca 2400
caggccgggg ctgcggtgca ggcacctggc catgctggct gggcgcccca 2450
agcacagccc tgactaggat gacagcagca caaaagacca cctttctccc 2500
ctgagaggag cttctgctac tctgcatcac tgatgacact cagcaggggtg 2550
atgcacagca gtctgcctcc cctatgggac tcccttctac caagcacatg 2600
agctctctaa cagggtgggg gctaccccca gacctgctcc tacactgata 2650
ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700
cagaaacaca gtgtttcaag agaccctaaa aaacctgcct gtcccaggac 2750
cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800
ctcctgaaa ctccactctg aagctgccgc tttggacacc aacactccct 2850
tctcccaggg tcatgcaggg atctgctccc tctgcttcc cttaccagtc 2900
gtgcaccgct gactcccagg aagtctttcc tgaagtctga ccacctttct 2950
tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000
caggggtaat ctgagccttc ttcactcctt taccctagct gacctttca 3050
cctctccccc tcccttttcc tttgttttgg gattcagaaa actgcttgtc 3100
agagactgtt tattttttat taaaaatata aggcttaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

	290		295		300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro		
	305		310		315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val		
	320		325		330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu	Asp		
	335		340		345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu		
	350		355		360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg		
	365		370		375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr		
	380		385		390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr		
	395		400		405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val		
	410		415		420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr		
	425		430		435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly		
	440		445		450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp		
	455		460		465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala		
	470		475		480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala		
	485		490		495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg		
	500		505		510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu		
	515		520		525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg		
	530		535		540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser		
	545		550		555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala		
	560		565		570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala		
	575		580		585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggctcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtcctt agccgggagc agggcgcgca gccaggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgttct tctagtgggc 100
ttccttctcc ctggggctct gctctcagag gctgccaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaagagaa ctgcgacatg gtgatagtgtg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctagga cagttttgtc tcatcttcta ctgaaagcag 800
agttgtgggt cattaactct gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200
 catccagcat ggtgtgcccc tgggtgggat ccctctcttt ggagaccagc 1250
 ctgaaaacat ggtccgagta gaagccaaaa agtttggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct cttaatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcctcctgc 1400
 gctcccaccc gctcagcccc acacagcggc tgggtgggtg gattgaccac 1450
 gtcctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550
 tcactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600
 tgggtggctgc gtggggccag aaaggtgaag gagacataag gccaggtgca 1650
 gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700
 cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750
 tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800
 attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850
 ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950
 aaaatccacc ttctttctca tgcgcctctc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctggtgcccc cagtgaagctc cttcttggct gagcaggcat 2250
 ggagactgta ggtttccaga tttctgaaa aataaaaagt tacagcgtta 2300
 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tgttctccat ccccccaggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
 ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggctacc 500
 aggtcccccata cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
 tgggggcccgg gtgggcccag gaggggtcag agcccgtcct gctggagggg 600
 gagtgcctgg tggctctgtga gcctggccga gctgctgcag gggggcccgg 650
 gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccacatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gaccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttctcttg ccctctcttg 1150
 cccagaaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggcctttc caccacaoca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttcct gcctgcagcc ctaggatcag 1350
 ggcaagggtt ggcaagaagg aagatctgca ctactttgag gcctctgctc 1400
 ctccggttcc cccacccag cttcctgctc aatgctgac agggacaggt 1450
 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttcctgtgag gaaagccagc atcacggatc 1550
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600
 aggtcagcc acaggcagaa ggggtgggaag ggctggagt ctgtggctgg 1650
 tgaggaagga aggagggtgt attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccctctat 1750
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acotttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctcctcctt aggcctccta ttacctggga ttccatgatt 2100
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgtact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50
 tagccgccca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc agtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcgagg atggggggccg ggggcggcgcg gcgcgcgact cgctgaggcc 50
ccgacgcagg gccggggccgg gccagggcc gaggagcgcg gcggccagag 100
cggggcccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
caccgcctcc tgagcagcg catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggcg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggctcatg ctgctggagt ggtggctcctg cacggagtgt acactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gogcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtggc actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgagagg 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggt 850
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
atgtaaccct gaacttcaga ggaacaaga acccgctcct gctggggatc 1000
ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200
 cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300
 tttgtgggag cagcttcott tggagttohc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaacia 1450
 aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaaga tggtagcttg agatttttca ggctaataa aaaagaatga 1600
 aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct cattttctct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtottagatg gtccctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcott gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggg tgatctcaaa ctctgagtt caggatgatc gcccgctca 2200
 gcctcccaaa gtgttgtgat tgcaggcgtg agccactgag cctggccgga 2250
 atttcttttt aaggctgaat gatggggggc aggcacgatg gctcacgcct 2300
 gtgatcccaa gtagcttgga ttgtaaacat gcaccacat gcctggctaa 2350
 tttttgtatt ttagtagag acgtgttagc caggctggtc tcgatctcct 2400
 gacctcaagt gaccacctgc ctgagcctcc caaagtactg ggattacagg 2450
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gccaggttg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggtgagg caggctgac 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtga actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
 1 5 10 15
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
 65 70 75
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
 80 85 90
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
 95 100 105
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
 110 115 120
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
 125 130 135
 Cys Gly Val Leu Leu Ser Phe Leu

```
<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens
```


Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
Leu	Thr	Leu	Ala	Phe	Lys	Ile									260		

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50

ctctcgccgt cagcatgccca cacgccttca agcccgggga cttggtgttc 100

gctaagatga agggctaccc tctactggcct gccaggatcg acgacatcgc 150

ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200

gcacacacga aacagccttc ctggggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
 cgccagttag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcaagtacg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcatctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
 cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750
 gtcagcctcc gactccgact ccaaggccga ttccggacggg gccaaagcctg 800
 agccggtggc catggcgcgg tcggcgctct cctcctcctc ttcctcctcc 850
 tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
 agcggagaag cctctcccga agccgcgagg gcggaaaccg aagcctgaac 950
 ggctccgctc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000
 atcagttagt ggaagcgcgg ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcggcgg cgagagcagg aggaggagct gcggcgccctg cgggagcagg 1100
 agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150
 gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200
 gcccgctcaag aagcggggac gcaagggccg gggccgggggt ccccgctcct 1250
 cctctgactc cgagcccag gccgagctgg agagagaggc caagaaatca 1300
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400
 aggtggagcg gacccggaag cggtcggagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagttagatc aagtttgccc taaaggtcga cagcccggac gtgaagaggt 1550
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttgccgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

	140		145		150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met Ser			
	155	160			165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala			
	170	175			180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser Glu			
	185	190			195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala			
	200	205			210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys			
	215	220			225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp Ser			
	230	235			240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser			
	245	250			255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser Val			
	260	265			270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro			
	275	280			285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser Ser			
	290	295			300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu			
	305	310			315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala Arg			
	320	325			330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln			
	335	340			345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly			
	350	355			360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg			
	365	370			375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly			
	380	385			390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu			
	395	400			405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser			
	410	415			420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg			
	425	430			435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	455	460	465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	470	475	480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	530	535	540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	545	550	555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	560	565	570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	575	580	585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					665	670	

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50

cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100

ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250
 tacaaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350
 tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400
 aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
 attatgtaaa ttagctggga aagatgccaa tacagaatgt gcaaatttca 500
 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550
 ggagcatttc atccaatatg tgggtatatt gatcttgag tctacaagga 600
 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650
 aatgtccttt cgatectcag cagccttttg cttcagtaat gacagatgag 700
 tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750
 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800
 tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850
 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900
 tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950
 ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000
 aagtggacga cttttcttaa ggccagactg atttgctcaa ttcttggaag 1050
 tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100
 ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150
 agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200
 cagagcagtt tttaatggct catatgctca taaggaaagt gcagaccatc 1250
 gttgggtgca gtatgatggg agaattcctt atccacggcc tggtagatgt 1300
 ccaagcaaaa cctatgaccc actgattaag tccacccgag attttocaga 1350
 tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccttat 1400
 acccagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450
 ctgacacaga tagtggtgga tcatgtcatt gcagaagatg gccagtacga 1500
 tgtaatgttt cttggaacag acattggaac tgcctcaaa gttgtcagca 1550

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
				125					130					135					
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
				140					145					150					
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
				155					160					165					
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
				260					265					270					
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

	665		670		675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
680	685				690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
695	700				705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715				720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730				735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745				750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
755	760				765
Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
770	775				

<210> 311
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 311
 caacgcagcc gtgataaaca agtgg 25

<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 312
 gcttggacat gtaccaggcc gtgg 24

<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 313
ggccagactg atttgc tcaa ttcctggaag tgatggggca gatac 45

<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

<400> 314
ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50
gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100
agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150
ctcagcagtt tcagccagca gggactgac aggtgtgtgt cctggagtgg 200
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300
gggtgaggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350
gaagagctga gagaggggat cttggagcca ttgaggggtgt catggagcta 400
cagaggggag ggaaaggtat tttaaggtaa cagtgtggca caatagttaa 450
gagcacagtt tttggagcta gaccgacata ggttcaaatt ctcttctgtt 500
gcttcctagt tctgtagccc caggtaaggg agtgacttaa cctctctgga 550
cttcaatttc ctcatcacta aagtagggcc aataatagca cccacctcat 600
agggagatt aaatgacata atgtatgtga tgcaactagc aaagtaccag 650
tcccatagta agtcatgccc cacagtattt ccacccaccc ctgttctctg 700
ccttcccaac cagggtactgc aacgactgga gcagaggcgg cagcaggctt 750
cagagcggga ggctccaagc atagaacaga gggtacagga agtgcgagag 800
agcatccgcc gggcacaggt gagccaggtg aagggggctg ccgggtggc 850
cctgctgcag ggggctggct tagatgtgga gcgctggctg aagccagcca 900
tgaccagcgc ccaggatgag gtggagcagg agcggcggct cagtgaggct 950
cggtgtccc agagggacct ctctccaacc gctgaggatg ctgagctttc 1000
tgactttgag gaatgtgagg agacgggaga gctctttgag gagcctgccc 1050
cccaagccct ggccacgagg gccctcccct gccctgcaca cgtgggtattt 1100
cgctatcagg cagggcgtga ggatgagctg acaatcacgg agggtgagtg 1150
gctggaggtc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200
accgacagc gcaggtaggc tttgtccctg agcgatatct caacttcccg 1250

agtttactct gggggttcag ggagccgaaa ggcttaaata gtttaagtag 2750
 gtgatgggaa gatgagatta cctcatttag ggctcaggca gactcacctc 2800
 acatactccc tgctccctgt ggtagagaca cctgagagaa aggggagggg 2850
 tcaacaatga gagaccagga gtaggtccta tcagtgtccc ccagagtaga 2900
 gagcaataag agcccagccc agtgcagtcc cggctgtgtt ttcctacctg 2950
 gtgatcagaa gtgtctggtt tgcttggtg cccatttgcc tcttgagtgg 3000
 gcagccctgg gcttgggccc ctccctccgg cctcagtgt tggtctgca 3050
 gaagctctgg ggttcccttc aagtgcacga ggggttaggc tgctgtccct 3100
 gagtcccca ttctgtactg gggggctggc taggacctgg ggctgtggcc 3150
 tctcaggggg cagcctctcc atggcaggca tccctgcctt gggctgccct 3200
 ccccagacc cctgaccacc cctgggtcc tgtccccac cagagcccca 3250
 gctcctgtct gtgggggagc catcacggtg ttcgtgcagt ccatagcgct 3300
 tctcaatgtg tgtcaccggg aacctgggag gggaggggaa actgggggtt 3350
 aggaccacaa ctcagaggct gcttggccct cccctctgac caggacatc 3400
 ctgagtttgg tggctacttc cctctggcct aaggtagggg aggccttctc 3450
 agattgtggg gcacattgtg tagcctgact tctgctggag ctcccagtcc 3500
 aggaggaaag agccaaggcc cacttttggg atcaggtgcc tgatcactgg 3550
 gccccctacc tcagcccccc tttccctgga gcacctgcc cacctgcca 3600
 cagagaacac agtggctctc cctgtccggg ggcgggtttt tccttccttg 3650
 gagcgtccct gacggacaag tggaggcctc ttgctgcggc tgcaatggat 3700
 gcaaggggct gcagagccca ggtgcactgt gtgatgatgg gagggggctc 3750
 cgtcctgcag gctggaggtg gcatccacac tggacagcag gagggggga 3800
 gtgagggtaa catttccatt tcccttcatg ttttgtttct tacgttcttt 3850
 cagcatgctc cttaaaaccc cagaagcccc aatttcccca agccccattt 3900
 tttcttgtct ttatctaata aactcaatat taag 3934

<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met	Gln	Leu	Ala	Lys	Tyr	Gln	Ser	His	Ser	Lys	Ser	Cys	Pro	Thr
1				5					10					15

Val	Phe	Pro	Pro	Thr 20	Pro	Val	Leu	Cys	Leu 25	Pro	Asn	Gln	Val	Leu 30
Gln	Arg	Leu	Glu	Gln 35	Arg	Arg	Gln	Gln	Ala 40	Ser	Glu	Arg	Glu	Ala 45
Pro	Ser	Ile	Glu	Gln 50	Arg	Leu	Gln	Glu	Val 55	Arg	Glu	Ser	Ile	Arg 60
Arg	Ala	Gln	Val	Ser 65	Gln	Val	Lys	Gly	Ala 70	Ala	Arg	Leu	Ala	Leu 75
Leu	Gln	Gly	Ala	Gly 80	Leu	Asp	Val	Glu	Arg 85	Trp	Leu	Lys	Pro	Ala 90
Met	Thr	Gln	Ala	Gln 95	Asp	Glu	Val	Glu	Gln 100	Glu	Arg	Arg	Leu	Ser 105
Glu	Ala	Arg	Leu	Ser 110	Gln	Arg	Asp	Leu	Ser 115	Pro	Thr	Ala	Glu	Asp 120
Ala	Glu	Leu	Ser	Asp 125	Phe	Glu	Glu	Cys	Glu 130	Glu	Thr	Gly	Glu	Leu 135
Phe	Glu	Glu	Pro	Ala 140	Pro	Gln	Ala	Leu	Ala 145	Thr	Arg	Ala	Leu	Pro 150
Cys	Pro	Ala	His	Val 155	Val	Phe	Arg	Tyr	Gln 160	Ala	Gly	Arg	Glu	Asp 165
Glu	Leu	Thr	Ile	Thr 170	Glu	Gly	Glu	Trp	Leu 175	Glu	Val	Ile	Glu	Glu 180
Gly	Asp	Ala	Asp	Glu 185	Trp	Val	Lys	Ala	Arg 190	Asn	Gln	His	Gly	Glu 195
Val	Gly	Phe	Val	Pro 200	Glu	Arg	Tyr	Leu	Asn 205	Phe	Pro	Asp	Leu	Ser 210
Leu	Pro	Glu	Ser	Ser 215	Gln	Asp	Ser	Asp	Asn 220	Pro	Cys	Gly	Ala	Glu 225
Pro	Thr	Ala	Phe	Leu 230	Ala	Gln	Ala	Leu	Tyr 235	Ser	Tyr	Thr	Gly	Gln 240
Ser	Ala	Glu	Glu	Leu 245	Ser	Phe	Pro	Glu	Gly 250	Ala	Leu	Ile	Arg	Leu 255
Leu	Pro	Arg	Ala	Gln 260	Asp	Gly	Val	Asp	Asp 265	Gly	Phe	Trp	Arg	Gly 270
Glu	Phe	Gly	Gly	Arg 275	Val	Gly	Val	Phe	Pro 280	Ser	Leu	Leu	Val	Glu 285
Glu	Leu	Leu	Gly	Pro 290	Pro	Gly	Pro	Pro	Glu 295	Leu	Ser	Asp	Pro	Glu 300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala

ctcacatcct	acgccggaag	agtcctgccca	gcggtcaagg	tcccatgtgc	1000
aacgtcaagg	ctcctcttgg	aagccccagc	cccagacccc	gaagagccaa	1050
gcgctttgct	tcactgagta	gattttgtgga	gacactgggtg	gtggcagatg	1100
acaagatggc	cgcattccac	ggtgcggggc	taaagcgcta	cctgctaaca	1150
gtgatggcag	cagcagccaa	ggccttcaag	cacccaagca	tccgcaatcc	1200
tgtcagcttg	gtggtgactc	ggctagtgat	cctgggggtca	ggcgaggagg	1250
ggccccaagt	ggggcccagt	gctgcccaga	ccctgcgcag	cttctgtgcc	1300
tggcagcggg	gcctcaacac	ccctgaggac	tcggggccctg	accactttga	1350
cacagccatt	ctgtttaccc	gtcaggacct	gtgtggagtc	tccacttgcg	1400
acacgctggg	tatggctgat	gtgggcaccg	tctgtgaccc	ggctcggagc	1450
tgtgccattg	tggaggatga	tgggctccag	tcagccttca	ctgctgctca	1500
tgaactgggt	catgtcttca	acatgctcca	tgacaactcc	aagccatgca	1550
tcagtttgaa	tgggcctttg	agcacctctc	gccatgtcat	ggcccctgtg	1600
atggctcatg	tggatcctga	ggagccctgg	tccccctgca	gtgcccgctt	1650
catcactgac	ttcctggaca	atggctatgg	gcactgtctc	ttagacaaac	1700
cagaggctcc	attgcatctg	cctgtgactt	tccctggcaa	ggactatgat	1750
gtgaccgccc	agtgccagct	gaccttcggg	cccgactcac	gccattgtcc	1800
acagctgccg	ccgccctgtg	ctgccctctg	gtgctctggc	cacctcaatg	1850
gccatgccat	gtgccagacc	aaacactcgc	cctggggccga	tggcacaccc	1900
tgcgggcccc	cacaggcctg	catgggtggg	cgctgcctcc	acatggacca	1950
gtccagggac	ttcaatattc	cacaggctgg	tggctggggg	ccttggggac	2000
catgggggtga	ctgctctcgg	acctgtgggg	gtggtgtcca	gttctcctcc	2050
cgagactgca	cgaggcctgt	cccccggaat	ggtggcaagt	actgtgaggg	2100
ccgccgtacc	cgcttccgct	cctgcaacac	tgaggactgc	ccaactgggt	2150
cagccctgac	cttcgcgcgag	gagcagtgtg	ctgcctacaa	ccaccgcacc	2200
gacctcttca	agagcttccc	agggcccatg	gactgggttc	ctcgctacac	2250
aggcgtggcc	ccccaggacc	agtgcaaact	cacctgccag	gcccgggcac	2300
tgggctacta	ctatgtgctg	gagccacggg	tggtagatgg	gacccctgt	2350
tccccggaca	gctoctcggt	ctgtgtccag	ggccgatgca	tccatgctgg	2400

ctgtgatcgc atcattggct ccaagaagaa gtttgacaag tgcattggtgt 2450
 gcggagggga cggttctggt tgcagcaagc agtcaggctc cttcaggaaa 2500
 ttcaggtagc gatacaacaa tgtggtcact atccccgcgg gggccacca 2550
 cattcttgct cggcagcagg gaaaccctgg ccaccggagc atctacttgg 2600
 ccctgaagct gccagatggc tcctatgccc tcaatggtga atacacgctg 2650
 atgccctccc ccacagatgt ggtactgcct ggggcagtca gcttgcgcta 2700
 cagcggggcc actgcagcct cagagacact gtcaggccat gggccactgg 2750
 cccagccttt gacactgcaa gtcctagtgg ctggcaacc ccaggacaca 2800
 cgcctccgat acagcttctt cgtgccccgg ccgaccctt caacgccacg 2850
 cccactccc caggactggc tgcaccgaag agcacagatt ctggagatcc 2900
 ttggcgggcg cccctgggcg ggcaggaaat aacctacta tcccggctgc 2950
 cctttctggg caccggggcc tcggacttag ctgggagaaa gagagagctt 3000
 ctgttgctgc ctcatgctaa gactcagtgg ggaggggctg tgggcgtgag 3050
 acctgcccct cctctctgcc ctaatgcgca ggctggccct gccctggttt 3100
 cctgccctgg gaggcagtga tgggttagtg gatggaagg gctgacagac 3150
 agccctccat ctaaactgcc ccctctgccc tgcgggtcac aggagggagg 3200
 ggaaggcag ggagggcctg ggccccagtt gtatttattt agtatttatt 3250
 cacttttatt tagcaccagg gaaggggaca aggactaggg tcctggggaa 3300
 cctgaccct gaccctcat agccctcacc ctggggctag gaaatccagg 3350
 gtggtggtga taggtataag tgggtgtgt atgctgtgt gtgtgtgtgt 3400
 gaaaatgtgt gtgtgcttat gtatgaggta caacctgttc tgctttcttc 3450
 ttctgaatt ttattttttt ggaaaagaaa agtcaagggt aggggtgggc 3500
 ttcagggagt gagggattat cttttttttt ttttctttct ttctttcttt 3550
 tttttttttg agacagaatc tcgctctgtc gccaggctg gagtgcaatg 3600
 gcacaatctc ggctcactgc atcctccgcc tcccgggttc aagtgattct 3650
 catgcctcag cctcctgagt agctgggatt acaggctcct gccaccacgc 3700
 ccagctaatt tttgttttgt tttgtttgga gacagagtct cgctattgtc 3750
 accagggctg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800
 cagcaattct cctgcctcag cctcccagat agctgagatt ataggcacct 3850

accaccacgc cgggctaatt tttgtatatt tagtagagac ggggtttcac 3900
catgttggcc aggctggtct cgaactcctg accttaggtg atccactcgc 3950
cttcatctcc caaagtgtcg ggattacagg cgtgagccac cgtgcctggc 4000
cacgccaac taatTTTTgt atTTTtagta gagacaggtt ttcacatgt 4050
tgGCCaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcgg 4100
cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccggtacata 4150
TTTTTTaaat tgaattctac tatttatgtg atccttttgg agtcagacag 4200
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300
aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400
aaggaaa 4407

<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
1 5 10 15
Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu	155		160		165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile	170		175		180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn	185		190		195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala	200		205		210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val	215		220		225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	230		235		240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His	245		250		255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val	260		265		270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala	275		280		285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn	290		295		300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu	305		310		315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu	320		325		330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	335		340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala	350		355		360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys	365		370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val	380		385		390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser	395		400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr	410		415		420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro	425		430		435

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp					
	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro					
	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys					
	830		835		

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttta atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgttttgga tcctggccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350
aaacattgga agtcacagac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttctact ttcttgccaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750
gaccgcgtcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcactctgtc tgatcatcat ccttgtaact ggtgggtggc cogcatgctg 1000
gggaggggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcactctg 1100
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1				5					10					15	
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50
caggagactg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
ggcgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcaactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
tggcgtgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350
tgcctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
cacgcgctgc gccaaaggca caccgcgcaa gaccaccttt gccatcctcg 450
gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550
cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
cgtccctctc gtcattggt ggcacctgc tttgcctgtc ctgccaggac 650
gaggcaccct acaggcccta ccaggccccg cccaggggcca ccacgaccac 700
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttgga 1100
gtttggctcag tgggggttgg ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
1 5 10 15
Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
20 25 30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
35 40 45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
50 55 60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
80 85 90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgctg 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacg catgctgcag gcagtgcgag cctgatgat cgtaggcatc 350
 gtcttgggtg ccattggcct cctggatatc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaaca 550
 gtacaccggc atgggtggga tggcgagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 ggggggtgtga tgatgtgcat cgctgcccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgtgtgt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcggttc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttoga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atgcgacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaaact ttgatttact gttcttaact gcctaactct aattacagga 900
 actgtgcac cagctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacct aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctacataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgctttttcag ggaaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc cattttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgctttttc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtottgggt ttcatittgt taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atctttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaaat actgtatttt totgttttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328

<211> 225

<212> PRT

<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
 tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50
 ctgggctggg tgaatggcct ggtctcctgt gccctgcca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgctgt gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgtctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgcttgggtgc tcacctctgg gattgtcttt gtcattctcag gggctcctgac 400
 gctaattccc gtgtgctgga cggcgcacgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg gggtgctgtg 550
 ctgcaacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg gggtcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
 tctggatott gacatgcca tcttagaagc cagtcaagct atggaactaa 950
 tgcgaggget gcttgctgtg ctggccttgc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atcctactca ggtctctgga gtcctctct tcacccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaactttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

gccccctcg tctcaccccc tttaactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50

atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100

ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150

agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200

tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250

gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300

aaatttcca tggacataga gagaaaggaa tgatattctc atcatcatct 350

tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400

ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgacctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgtc agggaccca acgcatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcagggtgc gactcatcta ccaagggcag ctgctaggog acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcg ggggtccgag 650
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttcccctgac cgccactctg ggcttgccg gcttccact gctcctcagt 800
 ctctggcct ttgccatgta ccgcccgtag tgctccgcg ggcgcttggc 850
 agcgtcgccg gcccctccg accttgctcc ccgcgcgcg gcgggagctg 900
 ctgcctgcc aggccgcct ctccggcctg cctcttcccg ctgcctgga 950
 gccagccct gcgcgcaga ggactcccgc gactggcgga gggcccgccc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100
 gccccgggca gagccgggccc gccccggggg ccggtcttag tgttctgccg 1150
 gaggaccag ccgcctcaa tccctgacag ctcttgggc tgagttgggg 1200
 acgccaggtc ggtgggaggc tggtgaaggg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
 aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtogct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacctatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catgttgcaa 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tcctgctgct cctgatgctg ggatgogtcc tgatgatggg 550
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650
tcccaggatt gggactgga agctgaggat gaggggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcact gggggaggat cagctgctgg 750
tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900
aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950
agtgcccgca tccccctcca gagggctctg cccgaggtgc ggcaccact 1000
gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
tctgtttcca tgatgaggcc tggteccact tcctgcggaac tgtacacagc 1100

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
 cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
 ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
 tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtg 200
 caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
 ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
 cctggcactg cacccccagc caccocatca ggctttgagg agggggccgc 350
 ctcatcccaa taccctggg ctatcgtgtg ggggtccacc gtgtctcgag 400
 aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggt 450
 tttgcagccc ctcatgggct cgcaacccca caccocaaact cagactccat 500
 gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
 ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
 gtcacaatta ccatctccat catcattgtt ctctgtggcca ctggcatcat 650
 cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
 agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
 tccccggctg gagtactgt gctgggggcc ttoggggact cacctacccc 800
 caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
 accccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
 tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
 tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000
 gccctggcc ctcccaaggg ggctggacca gctcctctct gggaggcacc 1050
 cttccttctc ccagtctctc aggatctgtg tcctattctc tgctgcccac 1100
 aactccaact ctgccctctt tggttttttc tcatgccacc ttgtctaaga 1150
 caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200
 ttctattctg gcctaccocct tggttcctga ctgtgccctt tccctcttcc 1250
 tctcaggatt cccctgggtga atctgtgatg cccccaatgt tggggtgcag 1300

ccaagcagga	ggccaagggg	cgggcacagc	ccccatccca	ctgagggtgg	1350
ggcagctgtg	gggagctggg	gccacagggg	ctcctggctc	ctgccccctg	1400
cacaccaccc	ggaacactcc	ccagccccac	gggcaatcct	atctgctcgc	1450
cctcctgcag	gtggggggcct	cacatatctg	tgaattcggg	tccctgtccc	1500
cacccttgtg	cactcacatg	aaagccttgc	acactcacct	ccaccttcac	1550
aggccatttg	cacacgctcc	tgcaccctct	ccccgtccat	accgctccgc	1600
tcagctgact	ctcatgttct	ctcgtctcac	atttgactc	tctccttccc	1650
acattctgtg	ctcagctcac	tcagtgggtca	gcgtttcctg	cacactttac	1700
ctctcatgtg	cgttttcccg	cctgatgttg	tgggtggtg	cggcgtgctc	1750
actctctccc	tcatgaacac	ccaccacact	cgtttccgca	gcccctgcgt	1800
gctgctccag	agggtgggtg	gaggtgagct	gggggctcct	tgggccctca	1850
tcggtcatgg	tctcgtccca	ttccacacca	tttgtttctc	tgtctcccca	1900
tcctactcca	aggatgccgg	catcaccctg	agggctcccc	cttgggaatg	1950
gggtagtgag	gccccagact	tcacccccag	cccactgcta	aaatctgttt	2000
tctgacagat	gggttttggg	gagtcgcctg	ctgcactaca	tgagaaaggg	2050
actcccattt	gcccttccct	ttctcctaca	gtcccttttg	tcttgtctgt	2100
cctggctgtc	tgtgtgtgtg	ccattctctg	gacttcagag	ccccctgagc	2150
cagtcctccc	ttcccagcct	ccctttgggc	ctccctaact	ccacctaggc	2200
tgccagggac	cggagtcagc	tggttcaagg	ccatcgggag	ctctgcctcc	2250
aagtctaccc	ttcccttccc	ggactccctc	ctgtcccctc	ctttcctccc	2300
tccttccttc	cactctcctt	ccttttgctt	ccctgccctt	tccccctcct	2350
caggttcttc	cctccttctc	actggttttt	ccaccttcct	ccttcccttc	2400
ttccctggct	cctaggctgt	gatatatatt	tttgatttat	ctctttcttc	2450
ttcttgtggt	gatcatcttg	aattactgtg	ggatgtaagt	ttcaaaattt	2500
tcaaataaaq	ccttttqcaq	ataa	2524		

<210> 352

 $\langle 211 \rangle$ 243

<212> PRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 353
<211> 480
<212> DNA
<213> Homo sapiens

<400> 353
gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg coctcactcc 50
cggccaggat ggcacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350
 tcgcgcctt gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5					10					15
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttggt tggcgccgg ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcgggccc gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccttg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggtat tccccaacg agctgcgaaa 400
catcttcgag gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca cccgcgggg acctccccta 550
agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
acgtcgctg ctttggctat aactgcgagt agggctcagg catcacacc 800
acctgtcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggctcccc ccttcacct ggctgtcatc gggtagggcg gggcgtggg 900
ttcaggggcg caccatttc aagcctgtgt cccacaggtc ctggcgag 950
tggaagtcag ctgtccagg cctcctgaac tacataaata actggcacia 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccgaggag gtggaacctc aaccagctc tgcgcaggag 1150
gcggtgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200
cgggcatctt tcctaaagg tcccatagg gtctggttcc acccatccc 1250
aggtctgtgg tcagagcctg ggagggttcc ctacgatgg taggggtgcc 1300
ccatggagg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
agaggagggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450
gggctctccc tatactggg acacctgctg gatgtcacct ctgcaaccac 1500
acctatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

150

```

<400> 357
agcaggagca ggagagggac aatggaagct gccccgtcca ggttcattgt 50
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatgtgt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggtatgaaa gaaaatggga aggtgatatc 650
atttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgccca cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctaact tatgcaaagt aaaaaggcac 900
aactcaaatc tcagagacac taaacaacag gatcactagg cctgcccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

```

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 359
 ccagcagtgc ccatactcca tagc 24

 <210> 360
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 360
 tgacgagtgg gatacactgc 20

 <210> 361
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 361
 gctctacgga aacttctgct gtgg 24

 <210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaaa gccgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcgtt gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttgggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcggggtga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttg gtagtggtg gcatagttac tgctgtggc ctaggtctca 700
ctctgctcat cagcatgatt ctggtgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggtta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg Ile Ser Trp	Ala Gly Asp Leu Asp	Lys Lys Asp Ala Ser Ile	110	115	120
Asn Ile Glu Asn	Met Gln Phe Ile His	Asn Gly Thr Tyr Ile Cys	125	130	135
Asp Val Lys Asn	Pro Pro Asp Ile Val	Val Gln Pro Gly His Ile	140	145	150
Arg Leu Tyr Val	Val Glu Lys Glu Asn	Leu Pro Val Phe Pro Val	155	160	165
Trp Val Val Val	Gly Ile Val Thr Ala	Val Val Leu Gly Leu Thr	170	175	180
Leu Leu Ile Ser	Met Ile Leu Ala Val	Leu Tyr Arg Arg Lys Asn	185	190	195
Ser Lys Arg Asp	Tyr Thr Gly Cys Ser	Thr Ser Glu Ser Leu Ser	200	205	210
Pro Val Lys Gln	Ala Pro Arg Lys Ser	Pro Ser Asp Thr Glu Gly	215	220	225
Leu Val Lys Ser	Leu Pro Ser Gly Ser	His Gln Gly Pro Val Ile	230	235	240
Tyr Ala Gln Leu	Asp His Ser Gly Gly	His His Ser Asp Lys Ile	245	250	255
Asn Lys Ser Glu	Ser Val Val Tyr Ala	Asp Ile Arg Lys Asn	260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

```

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggcc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgtc 250
gcctctggcc gagcggccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtacccat gtaaaccaga gacagttatg 500

```

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaaggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gatttttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75

Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaaaagaa gtctgggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggctt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100

gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaaagg actttggtgg tatctttcac acaaggatatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacgggt 300
 tcttcatcca ggaccagatt gctctgggtg agaggggggg ctgtctcctc 350
 ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggctga aagggagcc acaccactgg ccttcccttc 800
 cccagggccc ccaaggtgtg ctcatgctac aagaagaggc aagagacagg 850
 cccaggggt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgcccc tctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110						115					

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgtttctt ctttctggat gggggcccag gggggccagg agagtataaa 50

ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cactgttgcc 150

ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgct 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatgggc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctaccca gccaaaggagg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatacaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctagggtgg 650

ggatggggc catccgagct gaggccatct gtgtgggtgg ggctgatggg 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10					15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30

Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

atctcagaaa ttacaggaga taccctcaag tataatctgct gggttgcttag 700
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattoca agactgccgc 1050
 aacctggaac ttttgacctt gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcatg gaataaaatc agtgatcatag gacagaccat 1250
 gtcctggacc tggagctcct tacaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggacct agtggtttcc agtggtgtccc gaatctgcag 1350
 cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagtttttaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctctcatcc tgctggttat ctacgtgtca tggaagcgg accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac agggaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcaaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc caggagtggt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

				200					205					210
His	Leu	Glu	His	Asn 215	Gln	Phe	Ser	Lys	Leu 220	Asn	Leu	Ala	Leu	Phe 225
Pro	Arg	Leu	Val	Ser 230	Leu	Gln	Asn	Leu	Tyr 235	Leu	Gln	Trp	Asn	Lys 240
Ile	Ser	Val	Ile	Gly 245	Gln	Thr	Met	Ser	Trp 250	Thr	Trp	Ser	Ser	Leu 255
Gln	Arg	Leu	Asp	Leu 260	Ser	Gly	Asn	Glu	Ile 265	Glu	Ala	Phe	Ser	Gly 270
Pro	Ser	Val	Phe	Gln 275	Cys	Val	Pro	Asn	Leu 280	Gln	Arg	Leu	Asn	Leu 285
Asp	Ser	Asn	Lys	Leu 290	Thr	Phe	Ile	Gly	Gln 295	Glu	Ile	Leu	Asp	Ser 300
Trp	Ile	Ser	Leu	Asn 305	Asp	Ile	Ser	Leu	Ala 310	Gly	Asn	Ile	Trp	Glu 315
Cys	Ser	Arg	Asn	Ile 320	Cys	Ser	Leu	Val	Asn 325	Trp	Leu	Lys	Ser	Phe 330
Lys	Gly	Leu	Arg	Glu 335	Asn	Thr	Ile	Ile	Cys 340	Ala	Ser	Pro	Lys	Glu 345
Leu	Gln	Gly	Val	Asn 350	Val	Ile	Asp	Ala	Val 355	Lys	Asn	Tyr	Ser	Ile 360
Cys	Gly	Lys	Ser	Thr 365	Thr	Glu	Arg	Phe	Asp 370	Leu	Ala	Arg	Ala	Leu 375
Pro	Lys	Pro	Thr	Phe 380	Lys	Pro	Lys	Leu	Pro 385	Arg	Pro	Lys	His	Glu 390
Ser	Lys	Pro	Pro	Leu 395	Pro	Pro	Thr	Val	Gly 400	Ala	Thr	Glu	Pro	Gly 405
Pro	Glu	Thr	Asp	Ala 410	Asp	Ala	Glu	His	Ile 415	Ser	Phe	His	Lys	Ile 420
Ile	Ala	Gly	Ser	Val 425	Ala	Leu	Phe	Leu	Ser 430	Val	Leu	Val	Ile	Leu 435
Leu	Val	Ile	Tyr	Val 440	Ser	Trp	Lys	Arg	Tyr 445	Pro	Ala	Ser	Met	Lys 450
Gln	Leu	Gln	Gln	Arg 455	Ser	Leu	Met	Arg	Arg 460	His	Arg	Lys	Lys	Lys 465
Arg	Gln	Ser	Leu	Lys 470	Gln	Met	Thr	Pro	Ser 475	Thr	Gln	Glu	Phe	Tyr 480
Val	Asp	Tyr	Lys	Pro 485	Thr	Asn	Thr	Glu	Thr 490	Ser	Glu	Met	Leu	Leu 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacotca 100
gogatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggacctt ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacccggc gtttctccag ctcgatctgg aggetgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt ttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtggg tgctcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac ttacaataa 950
aagctctaca catTTTcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggg 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaaac actgaaaaac atggattcat ttctataaca catTTattta 1200
agtatataac acgttttttg gacaagtga gaatgtttta tcattctgtc 1250
atttgtttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
tttgcactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700
catatttggg ttaattttgc ttttattata ttgggtctagg aggaaggagc 1750
tttggagaat ggaactcttg aggactttag ccagggtgat ataataaagg 1800
tacttttgtg ctgcattaaa ttgcttgga agtgtttaaca ttatattata 1850
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
acocaaatct tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
atttcocctg tagcaaatct aattgccaca tgggtgcccta tatttcatag 2100
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10				15	

coatgcogtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
 atgggaaccc tctagctgtc attgggtccg gtgccttcgc ggggctggga 750
 ggcottacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800
 gccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850
 gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900
 tccctgcagg agctggacct ttccgggcacc aacctgggtgc ccctgcctga 950
 ggcgctgtc ctccacctcc cggcactgca gagcgtcagc gtgggcccagg 1000
 atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050
 ggctccagcc ccaaggtgcc cctgcactgc gtagacaccc gggaatctgc 1100
 tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
 aacagactgc tgtcctgggc tgccctcaggt cccgagtaac ttatgttcaa 1200
 tgtgccaaaca ccagtgggga gcccgaggc ctatgtggca gcgtcaccac 1250
 aggagtgtg ggcctaggag aggccttga cctgggagcc acacctagga 1300
 gcaaagtctc acccctttgt ctacgttgct tccccaaacc atgagcagag 1350
 ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400
 cttatccccc aagtgccttc cctcatgcct gggccggcct gaccgcgaat 1450
 gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtccac 1500
 tgggctgagt gtccccttgg gcccatggcc cagtcaactca ggggogagtt 1550
 tcttttctaa catagccctt tctttgccat gaggccatga ggcccgcttc 1600
 atccttttct atttcctag aaccttaatg gtagaaggaa ttgcaaagaa 1650
 tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700
 ggaaaaaggc taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750
 gcctcctgcc tcccagcccg gaccaatgc actttcttgt ctctctaat 1800
 aagccccacc ctccccgcct gggctcccct tgetgccctt gcctgttccc 1850
 cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
 gactctgggc ctctgaccag ctgtgcggca tgggctaagt caotctgccc 1950
 ttccggagcct ctggaagctt agggcacatt ggttccagcc tagccagttt 2000
 ctacccttg gttgggggtcc ccagcatcc agactggaaa cctaccatt 2050
 ttcccctgag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100

gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150
 ctggccctga gcacgacagc ctttcttacc ctcccaggaa tgccgtgaaa 2200
 ggagacaagg tctgcccagc ccatgtctat gctctacccc cagggcagca 2250
 tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300
 ttgttgccct tttaacggag tgtcactttc aaccggcctc ccctaccctt 2350
 gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaagggttga 2400
 tttgttcaact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450
 aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
 1 5 10 15
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu		350		

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggtatTTaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc toatgccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcacgac cccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
 tgattgtctt tatgcacccc caatcttaat tgagaccata cttgtataag 1100
 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10					15
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25					30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40					45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcocat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgaccc cttgggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcgatccc gttatcgtct tgcgtactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttgcca gaatgtgaat gtattgactg gaggagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata ttttttagca ctctgatcta caaatTTGga agaaccgaag 600
agctatggac ctgagatcac ttcttaagtc acatTTTcct tttgttatat 650
tctgtttgta gataggTTTT ttatctctca gtacacattg ccaaattggag 700
tagattgtac attaaatggt ttgtttcttt acatTTTTat gttctgagtt 750
ttgaaatagt tttatgaaat ttctttatTT ttcatTgcac agactgttaa 800
tatgtatata atacaagact atatgaattg gataatgagt atcagTTTTt 850
tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900
tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950
gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
ttttttggta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
<211> 158
<212> PRT
<213> Homo sapiens

<400> 410
Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15
Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30
Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60
Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tcctagataa ttttcggttg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cagctgtggc ggagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgttttaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctgggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag ccagacaca aacaaatagc agggatggcc agagctgctg 950
gagatggagg gctgcatgcc ccgaagcca ttttaggggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaagggtgct 1100
gcaggtcctt gcacgctgtg tcgctcctct cctcctcgga aacagaacct 1150
tcccacagca catcctacct ggaagaccag cctcagaggg tcttcttgga 1200
accagctgtc tgtggagaga atggggtgct ttogtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtcg cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gtcgctcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
at ttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

				80					85					90
Pro	Ser	Thr	Leu	Tyr 95	Leu	Gly	Gly	Leu	Pro 100	Arg	Lys	Tyr	Val	Ala 105
Ala	Gln	Leu	His	Leu 110	His	Trp	Gly	Gln	Lys 115	Gly	Ser	Pro	Gly	Gly 120
Ser	Glu	His	Gln	Ile 125	Asn	Ser	Glu	Ala	Thr 130	Phe	Ala	Glu	Leu	His 135
Ile	Val	His	Tyr	Asp 140	Ser	Asp	Ser	Tyr	Asp 145	Ser	Leu	Ser	Glu	Ala 150
Ala	Glu	Arg	Pro	Gln 155	Gly	Leu	Ala	Val	Leu 160	Gly	Ile	Leu	Ile	Glu 165
Val	Gly	Glu	Thr	Lys 170	Asn	Ile	Ala	Tyr	Glu 175	His	Ile	Leu	Ser	His 180
Leu	His	Glu	Val	Arg 185	His	Lys	Asp	Gln	Lys 190	Thr	Ser	Val	Pro	Pro 195
Phe	Asn	Leu	Arg	Glu 200	Leu	Leu	Pro	Lys	Gln 205	Leu	Gly	Gln	Tyr	Phe 210
Arg	Tyr	Asn	Gly	Ser 215	Leu	Thr	Thr	Pro	Pro 220	Cys	Tyr	Gln	Ser	Val 225
Leu	Trp	Thr	Val	Phe 230	Tyr	Arg	Arg	Ser	Gln 235	Ile	Ser	Met	Glu	Gln 240
Leu	Glu	Lys	Leu	Gln 245	Gly	Thr	Leu	Phe	Ser 250	Thr	Glu	Glu	Glu	Pro 255
Ser	Lys	Leu	Leu	Val 260	Gln	Asn	Tyr	Arg	Ala 265	Leu	Gln	Pro	Leu	Asn 270
Gln	Arg	Met	Val	Phe 275	Ala	Ser	Phe	Ile	Gln 280	Ala	Gly	Ser	Ser	Tyr 285
Thr	Thr	Gly	Glu	Met 290	Leu	Ser	Leu	Gly	Val 295	Gly	Ile	Leu	Val	Gly 300
Cys	Leu	Cys	Leu	Leu 305	Leu	Ala	Val	Tyr	Phe 310	Ile	Ala	Arg	Lys	Ile 315
Arg	Lys	Lys	Arg	Leu 320	Glu	Asn	Arg	Lys	Ser 325	Val	Val	Phe	Thr	Ser 330
Ala	Gln	Ala	Thr	Thr 335	Glu	Ala								

```
<210> 424
<211> 18
<212> DNA
<213> Artificial
```

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 cccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagagggc gcgcgggtga aaggcgcat t gatgcagcct gcggcggcct 50
 cggagcgcg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgct gagcgctct gagatcccca aggggaagca 250
 aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttat ttt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcaacttaaat gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgtaagaat tttttttata tctgttaa at aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 440
 gggtcgtgtt ttggagaga 19

<210> 441
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 441
 ctggccctca gagcaccaat 20

<210> 442
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 442
 tcctccatca cttcccctag ctcca 25

<210> 443
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 ctggcaggag ttaaagttcc aaga 24

<210> 444
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 aaaggacacc gggatgtg 18

<210> 445
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445
 agcgtacact ctctccaggc aaccag 26

 <210> 446
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 446
 caattctgga tgaggtggta ga 22

 <210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 447
 caggactgag cgcttggtta 20

 <210> 448
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 448
 caaagcgcca agtaccggac c 21

 <210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 449
 ccagacctca gccaggaa 18

 <210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 450
 ccctagctga ccccttca 18

<210> 451
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 451
 tctgacaagc agttttctga atc 23

 <210> 452
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 452
 ctctccccct cccttttctt ttgttt 26

 <210> 453
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 453
 ctctggtgcc cacagtga 18

 <210> 454
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 454
 ccatgcctgc tcagccaaga a 21

 <210> 455
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 455
 caggaaatct ggaaacctac agt 23

 <210> 456
 <211> 20
 <212> DNA

<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatggtctc gtcccatc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 472
 tcagggtcta catcagcctc ctgc 24

 <210> 473
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 473
 aaggccaagg tgagtccat 19

 <210> 474
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 474
 cctactgagg agccctatgc 20

 <210> 475
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 475
 tccaggtgga cccacttca gg 22

 <210> 476
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 476
 gggaggctta taggccaat ctgg 24

 <210> 477
 <211> 50
 <212> DNA
 <213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50